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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 16, 2004, 16:34:37; Search time 40 Seconds (without alignments) 1096.871 Million cell updates/sec Run on:

US-09-905-589A-2 2364 1 MRKISNHGSLRVAKVAYPLG......ALGAIFHYIDSLNRQKSPAS 456 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SS	Description	hypothetical prote		quanosine-diphosph	apyrase (EC 3.6.1.	nucleoside triphos	probable nucleosid	hypothetical prote					_		hypothetical prote	7A19,33 protein -	nucleoside-triphos	probable formate d	tail protein - Met	formate dehydrogen	hypothetical prote		cell-division prot	glutamyl tRNA-gln	heat shock protein	connectin/titin -	nitrate reductase	titin, cardiac mus	dihydrolipoamide d	H+-transporting tw
SUMMARIES	ID	T23508	T39109	A40732	JC4616	S48859	G84442	T34147	D86276	S50463	T16696	E86276	156242	T40856	T04439	C86276	A55421	C71007	T12737	E75124	T24948	T27308	I39847	G72274	G81346	T42633	T37045	138344	3	S17724
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	Length	479	556	518	454	455	516	485	483	630	557	405	510	572	1052	508	628	619	1186	999	322	322	440	475	623	4162	1233	26926	~	504
ako	Query Match	25.0	21.5	21.1	20.5	18.7	'n.	4	14.4	13.9	13.0	12.7	12.1	11.9	10.4	9.3	5.9	4.7	4.6	4.5	4.4	4.4	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2
	Score	9	508	498	485	442.5	372	343	339.5	329.5	307	301	285.5	281.5	245.5	219	140.5	111	108.5	106.5	104.5	103.5	102.5	102	102	102	100	100	99.5	•
	Result No.	П	7	æ	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

356 YYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSS----PFSCMDLTYV-SL 410

g δ

40 yo

dnaK-type molecula	tyrosine kinase su	DNAK Protein limpo	dnad protein (heat	adenosylhomocystei	triacylglycerol li	actinomycin synthe	probable efflux pr	DNA topoisomerase	hypothetical prote	hypothetical prote	protein W03D8.9 [i	heat shock transcr	triacyldlycerol li	cyclosporin synthe	nicotinic acid pho
I39585	A46299	AEZSYI	E9/3/3	C64473	S32615	T14591	T35970	873898	T25894	T32940	D87733	S25478	S2344B	S41309	F97119
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ALIGNMENTS

ns text_change 09-Jul-2004 N:CAB05544.1; GSPDB:GN00023; CESP:K0E	Length 479; Indels 25; Gaps 9; TrkavkpglsavabDVEKSaog 127 	FVESSEIMHLRELKGSPVYLFS 338
RESULT 1 T23508 Pypothetical protein K08H10.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T23508 A;Acacession: T23508 A,Accession: T23508 A,Accession: T23508 A,Accession: T23508 A,Accession: T23508 A;Reference number: Z19750 A;Reference number: Z19750 A;Residues: 1479 eMID-A;Accession: T23508 A;Residues: 1-479 eMID-A;Accession: T23508 A;Residues: 1-479 eMID-A;Caess-references: UNIPROT:Q9XU84; EMBL:Z83113; PIDN:CAB05544.1; GSPDB:GN00023; C;Genetics: C;Genetics: A;App position: 5 A;Introms: 36/3; 83/3; 189/1; 300/2; 412/3 C;Superfamily: nucleoside triphosphatase chromatin-associated	Query Match 25.0%; Score 590.5; DB 2; Length 479; Best Local Similarity 34.2%; Pred. No. 4.4e.40; Matches 134; Conservative 78; Mismatches 155; Indels 25; Gaps 73 FYGIMFDAGSTGTRVHVGPTRPRETPTLTHETFRAVREGLSAYADDVEKSAGG	281 MPEGYQLIEMEYALKFWNINGSSSHSFESCYGTIKNFVESSEIMHLRELKGSPVYLFS
RESULT 1 723508 hypothetical protein C,Species: Caenorhabd C,Date: 15-Oct-1999 # C,Accession: T23508 R,Gardner, A.Reference number: Z A,Reference number: Z A,Status: Preliminary A,Molecule type: DNA A,Resiques: 1-479 «WI A,Cross-references: U A,Experimental source C,Genetics: A,Gene: CSP: KOBHIO.4 A,Map position: 5 A,Introns: 36/3; 83/3 C;Superfamily: nucleo	Query Matches Matches Oy Oy Db OO Db OO OO OO OO OO OO OO	Db 28

C.; Wei, Y.; Taylor,

P.; Komp,

9871. and

8334,

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A; Cross-references: EMBL: U18779; NID: 9603625; PIDN: AAB65000.1; PID: 9603637; MIPS: YEL042w
                                                                                                                                                                                                                       A;Residues: 1-518 <MUL>
A;Cross-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65000.1; PID:g603637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A) Description: hydrolase
C; Superfamily: nucleoside triphosphatase chromatin-associated
C; Keyords: glycoprotein; Golgi apparatus; hydrolase; transmembrane protein
F; 10-24/Domain: transmembrane #status predicted <TMM>
F; 10-28/Domain: transmembrane #status predicted <TMM>
extracted from NCBI backbone (NCBIN:134708, NCBIP:134711)
                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmids 8199,
A; Reference number: S50491
                                                         A;Molecule type: protein
A;Residues: 125-144;238-257;276-281;366-374;399-412 <AB2>
R;Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl,
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SGD:GDA1
A;Cross-references: SGD:S0000768; MIPS:YEL042w
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A; Residues: 1-518 <DIE>
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94A0
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A,Residues: 1-556 <BAR>
A,Cross-references: UNIPROT:09UT35; EMBL:AL121741; PIDN:CAB57338.1; GSPDB:GN00066; SPDB:
A,Experimental source: strain 972h-; cosmid c824
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                                                                                                                      probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Acession: T3109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D. submitted to the EMBL Data Library, October 1999
A;Reference number: Z21828
A;Accession: T39109
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLD
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32.4%;
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142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 TKTHQLSSPCLPPKVNATNEKVTLESKETYTIDFIGPDEPSGAQ------CRFLTDEI 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQ------NRVHRTEEVKHV----DFYAFSYYYDLAAGVGLIDAEKGGSLVVGD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 LNKDAQCQSPPCSFNGVHQPSLVRTFKESNDIYIFSYFYDRTRPLGM-----PLSFTLNE 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QPQSSPFSCMDLTY-VSLLLQEFGFPRSKVLKL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 INDLARIVCKGEETWNSVFSGIAGSLDELESDSHFCLDLSFQVSLLHTGYDIPLQRELRT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apyrase (EC 3.6.1.5) precursor - potato
N'Alternate names: adenyl'pytrophosphatase; ATP-diphosphohydrolase
C.Species: Solanum tuberosum (potato)
C.Species: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                            122 EKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGIRLLPGEKAQKLLQKVKE-VFKASP
                                                                                                                                                                                                                                                                                  140 VGAANSLDPLLKVAMNYVPIKARSCTPVAVKATAGLRLLGDAKSSKILSAVRDHLEKDYP
                                                                                                                                                                                                                                                                                                                                                                                                           65 TAADGHEVFYGIMFDAGSTGTRVHVFQF---TRPPRETPTLTHETFKAVKPGLSAYADDV
                                                                                                                                                                                                                                                                                                                                                                     F-LVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGS--SVGMLDLGGGSTQIAFLPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SGOKAAASLHELCAARVSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 EGTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGK-----
                                                               Gaps
                                                               78;
Length 518;
   21.1%; Score 498; DB 2; Length 51 llarity 33.1%; Pred. No. 1.7e-32; Conservative 60; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ELVSPCLSPSFKGEWE----HAEVTYRV-
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Matches 125; Conservative
                     C; Accession: S65147; S48859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 IFHYIDSL 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 AVEAISAL 445
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-516 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: G84442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
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C;Accession: JC4616; PC4147

R;Anada, M.; Gudotti, G.

Biochem. Biophys. Res. Commun. 218, 916-923, 1996

A;Title: Purification and cloning of a soluble ATP-diphosphohydrolase (Apyrase) from pot A;Reference number: JC4616; MUID:96158985; PMID:8579614

A;Accession: JC4616

A;Molecule type: mRNA

A;Residues: 1-45 < AAN>

A;Cross-references: UNIPROT:P80595; GB:U58597; NID:g1381632; PIDN:AAB02720.1; PID:g13816
                                                                                                                                                                                                                                                                                                                                                                     the hydro
insensiti
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C;Superfamily: nucleoside triphosphatase chromatin-associated
C;Superfamily: nucleoside triphosphatase; transmembrane protein
C;Keywords: glycoprotein; hydrolase; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;1-31-454/Product: ATP-diphosphohydrolase #status predicted <MMT>
F;31-454/Product: ATP-diphosphohydrolase #status predicted <MMT>
F;44-65/Region: actin-heat shock protein 70-hexokinase beta-phosphate binding
F;192-212/Region: actin-heat shock protein 70-hexokinase gamma-phosphate binding
F;192-212/Region: nucleotide binding #status predicted
F;181,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                A;Note: The authors translated the codon GCA for residue 215 as Gly C;Comment: This enzyme belongs to a family of E-type ATPsses, and it catalyzes enzyme has nucleotide substrate specificity, divalent cation requirement, and olved in starch synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 YADDVEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 YABDPKAAANSLEPLLDGAEGVVPQELQSETPLELGATAGLRMLKGDAAEKILQAVRNLV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-ASPFLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 KNOSTFHSKDOWVTILDGTQEGSYMWAAINYLLGNLGKDYKSTTATIDLGGGSVQMAYAI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVEGTLQA----SPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELVSPCLSPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQ-NRVHRTEEVK--- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 VWNGGGGDGQKNIHASSFFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPPKTODRNIPYLCMDLIYEYTLLVDGFGLNPHKEITVIHDVQYKNYLVGAAWPLGCAID 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LETQPQSSPFSCMDLTY-VSLLLQEFGFPRSKVLKLTRKIDN----VETSWALGAIFH 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S48859
nucleoside triphosphatase precursor, chromatin-associated - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 AHSPLGTAADGHE-VFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTH-ETFKAVKPGLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 SNEQFAKAPQNEDGEPYVQQKHLMSKDYNLYVHSYLNYGQLAGRAEIF------KASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----HVDFYAFSYYYDLAAGVGLIDAEKGGSLVVG-DFEIAAKYVCRT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.5%; Score 485; DB 2; Length 45 31.9%; Pred. No. 1.6e-31; ive 68; Mismatches 183; Indels
                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 59-95;96-131;132-160;236-253;332-345 <HA2>
A; Experimental source: tubers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 YIDSLNRQKSPAS 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVSSTTNKIRVAS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 31.9
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
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C:Species: Arabidopsis thaliana (mouse_ear cress)
C:Date: 0.2-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C:Date: 0.2-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
R:Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.; eass, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                        PIDN:CAA83655.1; PID:g56361
                                                                                          chromatin
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A,Reference number: A84420, MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 YGIMFDAGSTGTRVHVFQFTRPPRETPTLTH-----ETFKAVKPGLSAYADDVEKSAQGI 128
                                                                                   calmodulin-regulated,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 LAGFNGIYTYSGEBFKATAYTSGANFNK------CKNTIRKALKLNYPCPYQNCTFG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSSPF-----SCMDLTYVSLLLOEFGFPRSKVLKLT--RKIDN----VETSWALGA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------VDFYAFSYYYDLAAGVGLIDAEKGGSLV-VGDFEIAAKYVCR-TLETQP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 STYPFLDKKNVASYVCMDLIYQYVLLVD-GFGLDPLQKITSGKEIEYQDAIVEAAWPLGN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 YAVVFDAGSTGSRIHVYHF----NONLDLLHIGKGVEYYNKITPGLSSYANNPEQAAKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 RELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVF-KASPFLVGDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 VSIIDGTQEGSYLWVTVNYALGNLGKKYTKTVGVIDLGGGSVQMAYAVSKKTAKNAPKV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ADGDDP-YIKKVVLKGIPYDLYVHSYLHFGREASRAEILKLTPRSP-----NPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 GIWNGGGGNGQKNLFASSSFFYLPEDTGWVDASTPNFILRPVDIETKAKEACALNFEDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 VSIMNGTDEGVSAWITINFLIGSLKTPGGSSVGMLDLGGGSTQIAF-----LPRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 GTLQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
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                                                                                                                                                                                                                                                                                                                                                                                             455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 SPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 516;
Fibility, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
Plant Mol. Biol. 30, 135-147, 1996
A;Title: Light-modulated abundance of an mRNA encoding a calmo A;Reference number: S65141; MUID:96197404; PMID:8616230
A;Accession: S65147
A;Molecule type: mRNA
A;Residues: 1-455 <HS2>
A;Cross-references: UNIPROT:P52914; EMBL:Z32743; NID:9563611; C;Superfamily: nucleoside triphosphatase chromatin-associated C;Keywords: nucleus
                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                  18.7%; Score 442.5; DB 2; 29.2%; Pred. No. 4.6e-28; ative 79; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 372; DB 2;
Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.7%;
29.0%;
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Best Local Similarity
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A;Map position: 2
C;Superfamily: nuc
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FORT———RPERETPLITHETEKAVKPGLGANYADDVEKSAQGIR 12	; Conservative /4; Mismatches 15/; HEVFYGIMPDAGSTGTRVHVFQFTRPPRETPTLTHE : :	21	<pre>Qy 122 EKSAQGIRELLDVAKQDIPFDFWKATFILVLAATAGLALLPGEKAQKLLDQKVENYFKASFF 181 </pre>	Qy 182 L-VGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 240	LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELV 29	Db 197 KESYNGGNVYEINLGSIETNEDYKYKIYSTTFLGYGANEGLKKYENSLVKSGNS 250 Qy 295 SPCLSPSFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEV 335

logic, boat, charge, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; N.F.; Hughes, B.; Huizar, L.

78. Hutter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C., J.; J. H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

2: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

3: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

3: Spreliminary

3: Sequence Source, Salary, MulD:21016719; PMID:11130712 references: UNIPROT: Q9X162; GB: AE005172; NID: g5080801; PIDN: AAD39311.1; GSPDB: GN 364 FLAT----ASFYYTAKFFELEEKGWLSELIPAGKRYCG--EEWSKLILEYPTIDEEYLR 416 304 KNYSSGFLADESKLKGSLQAAGNFSKCRSATFALLKEGKENCLYEHCSIGSTFTPDLOGS 363 340 VHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSP 399 291 KELVSPCLS--PSFKGEWEHA-----EVTYRVSGOKAAASLHELCA--ARVSEVLONR 339 388 CR----TLETQPQSSPF-----SCMDLTYVSLLLQEFGFPRSKVLKLTR---KID 430 74 YGIMFDAGSIGIRVHVFQF----IRPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIR 129 ELLDVAKODIPFDFWKATPLVLKATAGLRLLPGEKAQKLLOKVKEVFKASPFLVGDDCVS 189 IMNGIDEGVSAWITINFLIGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGILQASPPGYL 249 189 VISGSDEGIYSWITANYALGSLGTDPLETTGIVELGGASAQVTFV----SSEHVPPEYS 243 250 TALRMENRTYKLYSYSYLGLG-----LMSARLAILGGVEGOPA-----KDG 290 244 RIJAYGNISYIIYSHSFLDYGKDAALKKLLEKLQNSANSTVDGVVEDPCTPKGYIYDINS 303 -----LQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFFIAAKYV 387 ----SGGEYHYQKFIDEVRKY 346 ::| |:|| : --DVCLAQVSSLIGDKAQF 291 ical protein F7A19.34 [imported] - Arabidopsis thaliana ss. Arabidopsis thaliana (mouse-ear cress) 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 Gaps 55; DB 2; Length 483; 417 GYCFSAAYTISMLHDSLGIALDDESITYASKAGEK--HIPLDWALGA 461 400 FSCMDLTY-VSLLLQEFGFPR----SKVLKLTRKIDNVETSWALGA Indels iamily: nucleoside triphosphatase chromatin-associated Match
Local Similarity 26.5%; Pred. No. 1.2e-19;
es 108; Conservative 78; Mismatches 166; 292 SCPNPTCFLRNVIAPSVNLSTVQLYGFSEYWYTTSNFG-: || : || 251 NDSCSPRGLNRLIGEFTVNGTGEW 431 NVETSWALGAIFHYIDSL 448 406 GEEMQWALGAMLYHSKDL 423 sion: D86276 sition: 1 130

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C'Accession: E8626

R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

Ayuthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Ayuthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A; Althors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A; Fitle: Sequence and analysis of chromosome lof the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 ASAQIAFELPDTDSFSSINVENINLGCREDDSLFK--YKLFVTTFLGYGVNEGIRKYEHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVGDFEIAAKYVC----RTLETQPQSSPF-----SCMDLTYVSLLLQEFGFPRSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --EAHTSPKVIADDOER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 FYGIMFDAGSIGTRVHVFQFTRPP-----RETPTL--THETFKAVKPGLSAYADDVEKSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFLVGDDCVSIMNGTDEGVSAWITINFL-----TGSLKTPGGS-----SVGMLDLGG
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                         Indels 122;
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                                                                                   A;Gene: CESP:R07E4.4
A;Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2
                                                                                                                                                                                                                                                                                                                    88; Mismatches 178;
                                                                                                                                                                                                                            Query Match
13.0%; Score 307; DB 2;
Best Local Similarity 23.5%; Pred. No. 6.5e-17;
Matches 119; Conservative 88; Mismatches 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THNKFOSVSTIAGQEVQWALGAMIYHM 472
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Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AMIFFP----VIVFIYVV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.7%;
25.4%;
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A;Status: preliminary
A;Molecule type: DNA
                                  C; Genetics:
A; Gene: CESP: R07E4
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A;Residues: 1-630 <DIE>
A;Cross-references: UNIPROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00009
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A;Molecule type: DNA
A;Residues: 1-557 <MIL>
A;Cross-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4
                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda
A;Reference number: S50433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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FGIVIDAGSSGSRIHVFKW----QDTESLLHATNQDSQSILQSVPHIHQEKDWTFK-LNP 64
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                                                                                                                                                                                                        C.Species: Saccharomyces cerevisiae
C.bate: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
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                                                                                                                                                            hypothetical protein YER005w - yeast (Saccharomyces cerevisiae)
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R; Dietrich, F.S.
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A;Gene: SGD
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Db 334 NTSYCPYSQERGENEPELGGDFGAFSAFYFWAKENLIFSEKUSGEKV 382 Qy 377 VGDFBIAAKVCRTLETQPGSPFSCMDLTV-SILLQFFGFPRSKVLK 424	Query Match 11.9%; Score 281.5; DB 2; Length 572; Beet Local Similarity 2.1.4; Pred. No. 8e-15; Matches 111; Conservative 64; Mismatches-164; Indels 121; Gaps 15; Matches 111; Conservative 64; Mismatches-164; Indels 121; Gaps 15; Oy
Watches 104; Conservative 65; Mismatches 181; Indels 60; Gaps 13; 13; 14 VGIMPDAGSTGTRVHVPOFTRPPRETPILTHETRANKPGLSAXADDVEKSAQGIRELLD 133 4 FGYMFESGKPVEDFGEEHYASLKISPGLSSYADNPEGASVSTKLVF:	RESULT 12 Impublic cell activation antigen - human C.Species: Howo sapiens (multiple)

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Search completed: Nob time: 44 secs
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   Ribevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.; Mewes, submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15359
A;Accession: T04439
A;Accession: T0443
A;Residues: 1-1052 <BEV>
A;Residues: 1-1052 <BEV>
A;Cression: T0451
A;Experimental source: cultivar Columbia; BAC clone T18B16
C;Genetics: A;Antrons: 79/3; 118/3; 217/1; 295/3; 396/3; 531/2; 815/3
A;Note: T18B16.150
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7AL9-33 protein - Arabidopsis thaliana
(C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Accession: C86276
                                                                                                                                                                                                                                                                                         197 GVSAWITINFLTGSL-KTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMF
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                                                                                                                                                                                                                                                                                                                                                                                                                  603 KQIPKNAHRTTSLFVYATAGVRRLRPADSSWILGNVWSILAKSPFTCRREWVKIISGTEE
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                                                                                                                                                                                                                                            97;
                                                                                                                                                                                                              DB 2; Length 1052;
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                                                                                                                                                                                                        10.4%; Score 245.5; DB 2;
llarity 25.3%; Pred. No. 1.6e-11;
Conservative 60; Mismatches 185;
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                                                                                                                                                                                                                        Similarity
Accession: T04439
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Best Local S:
Matches 116,
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rrch completed: November 16, 2004, 17:00:26 time : 44 secs

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-508 <STO> A,Cross-references: UNIPROT:Q9XI63; GB:AE005172; NID:g5080800; PIDN:AAD39310.1; GSPDB:GN

Chin, C.W.; Chung, M.K.; Con, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Ref. M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C86276

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124
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                                                                                                                                                                                                                                                                                                           62 -VSLHYSVIIDGGSSGTRVHVFGY-RIESGKPVFDFGENYASLKLSPGLSAYADNPEGV
                                                                                                                                                                           9 SLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAHSPLGTAAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 BTQPQSSPFSCMDLTY-VSLLLQEFGFP-RSKVLKLTRKI--DNVETSWALGAI-----
                                                                                                                                       Gaps
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                                                                                                                                  Indels 100;
A;Map position: 1
C;Superfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                                                             83; Mismatches 196;
                                                                           / Match 9.3%; Score 219; DB 2; Local Similarity 22.3%; Pred. No. 8.3e-10; les 109; Conservative 83; Mismatches 196
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

November 16, 2004, 16:34:13 ; Search time 196 Seconds (without alignments) 1338.627 Million cell updates/sec

US-09-905-589A-2 2364 1 MRKISNHGSLRVAKVAYPLG......ALGAIFHYIDSLNRQKSPAS 456 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 Total number of hits satisfying chosen parameters:

1825181 segs, 575374646 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GDA1 SCHPO Q9XFC9	Q84UD8 O8RVT6	O9FUII O9SPM6	QCBK6	Q6FLR7	GDA1 YEAST	Q6Z4P2	BAC83798	Q753F2	AAS53733	Q98QG2
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32 33	3.4 3.5	36	38	39	40	41	42	43	44	45

ALIGNMENTS

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A Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Ehat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Ehat N.K.,
A Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J. Usdin T.B., Pondiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tookhyuki S., Carninci P., Prange C.,
A Rosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,
A Bosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,
A Holdon B., Ketteman M., Sodergren E.J., Lu X., Gibbs R.A.,
A Pahel J. Helton E., Ketteman M., Madan A.M., Roufigues S., Sanchez A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
A Pahes J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
B Hutterfield Y.S. N., Krzywinski M.I., Skalska U., Smallus D.E.,
B Hutterfield Y.S. N., Krzywinski M.I., Skalska U., Smallus D.E.,
B Homeration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUDMEDITULAR LOCATION, AND TISSUE SPECIFICITY.

SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

PubMed=11041856; DOI=10.1021/bi0009592;

Yeung G., Mulero J.J., McGowan D.W., Bajwa S.S., Ford J.E.;

redominantly expressed in the heart.";

Biochemistry 39:12916-12923 (2000).

-!- FUNCTION: Might support glycosylation reactions in the Golgi apparatus and, when released from cells, might catalyze the hydrolysis of extracellular nucleotides. Hydrolyses preferentially nucleoside 5'-diphosphates, nucleoside 5'-triphosphates are hydrolysed only to a minor extent, there is no hydrolysis of nucleoside 5'-monophosphates. The order of activity with different substrates is GDP > UDP = CDP >> ADP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    occurs in a soluble extracellular form.
TISSUE SPECIFICITY: Expressed in most tissues, but predominantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II membrane protein. Golgi. But also
SEQUENCE FROM N.A., AND SOLUBLE FORM DISULFIDE BONDS.
PubMed=14529283; DOI=10.1021/bi035137r;
Ivanenkov V.V., Murphy-Piedmonte D.M., Kirley T.L.;
"Bacterial expression, characterization, and disulfide bond determination of soluble human NTPDase6 (CD39L2) nucleotidase: implications for structure and function.";
Biochemistry 42:11726-11735(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide + phosphate.
COFACTOR: Requires calcium and magnesium (By similarity)
SUBCELLULAR LOCATION: Type II membrane protein. Golgi. B
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PROSITE; PS01238; GDA1_CD39 NTPASE; FALSE NEG.
Calcium, Glycoprotein; Golgī stack; Hydrolase; Magnesium;
Polymorphism; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MIM; 603160; -.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                     In soluble form.

In soluble form.

N-linked (GlONAc. ...) (Potential).

N-linked (GlONAc. ...) (Potential).

L -> V (in dbSNP:1044567).

/FIId=VAR_017863.
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                 membrane
                                                                                                                                                                                                                                                                                  Length 484;
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GO, GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000407; GDAl_CD39_NTPase.
                                                                                                                                                                                                                                                                                                                          Indels
           Signal-anchor for type II protein (Potential).
Lumenal (Potential).
                                                                                                                                                                                       S -> N (in Ref. 3).
Missing (in Ref. 4).
E -> K (in Ref. 2).
604C958953179089 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp761J1915 (Fragment).
Cytoplasmic (Potential)
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Pred. No. 1.6e-177;
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138
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                                                                                                                                                                                                                                                    484 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Braun N., Fengler S., Ebeling C., Servos J., Zimmermann H.;
Sequencing, functional expression and characterization of rat
NTPDase6, a nucleoside diphosphatase and novel member of the ecto-
nucleoside triphosphate diphosphohydrolase family.";
Biochem. J. 351:639-647(2000).
-! FUNCTION: Might support glycosylation reactions in the Golgi
apparatus and, when released from cells, might catalyze the
hydrolysis of extracellular nucleocides. Hydrolyses preferentially
nucleoside 5'-diphosphates, nucleocides Hydrolyses are
hydrolyzed only to a minor extent, there is no hydrolysis of
nucleoside 5'-monophosphates. The order of activity with different
substrates is GDP > IDP >> ADP. ADP.
-!- CATALYITY A nucleoside diphosphate + H(2)O = a
                                                                                                                         SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                                                                                                         LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                           1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
                                                                                                                                                                                                           VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
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                                                                                                                                                                                                                                                           FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION STRAIN-Sprague-Dawley, TISSUE-Brain; MEDLINE-20498744; PubMed=11042118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 41, Last annotation update)
Ectomucleoside triphosphare diphosphohydrolase 6 (EC 3.6.1.6)
(NTPDase6) (CD39 antigen-like 2).
                                                               Length 503;
                                                                                      Indels
                                    163933F9139D8D9F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
                                                           99.9%; Score 2361; DB 2;
99.8%; Pred. No. 1.7e-177;
iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455
                                  503 AA; 54763 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Entpd6; Synonyms=Cd3912;
Pfam; PF01150; GDA1 CD39;
                                                                                  Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat)
          Hypothetical protein.
NON TER 1
SEQUENCE 503 AA; 5
                                                                       Similarity
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                                                          Query Match
Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                  -!- COFACTOR: Requires calcium and magnesium.
-!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi. But also occurs in a soluble extracellular form.
-!- SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal-anchor for type II membrane protein (Potential).
Lumenal (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               In soluble form (By similarity).
In soluble form (By similarity).
In soluble form (By similarity).
N-linked (GlcNAc. .) (Potential)
N-Linked (GlcNAc. .) (Potential)
19A22E8BAEFOF7TB CRC64;
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                                                                                                                                                                                                                                                                                                                                           EMBL; AJ277748; CAC16598.1; -...
RGD; 619725; Entpd6.
InterPro; IPR00407; GDA1_CD39_NTPase.
Pros; Froils0; GDA1_CD39_INPASE.
PROS; Fre Se01239; GDA1_CD39_NTPASE; FALSE NEG.
Calcium; Glycoprotein; Golgī stack; Hydrolase; Magnesium;
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                                                                                                                                                                                                                                                                           entities requires a license agreement (St or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49899 MW;
nucleotide + phosphate.
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Matches 394; Conservative
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                                                                                                          Euteleostomi;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Bctonucleoside triphosphate diphosphohydrolase 6.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB=Brain;
Mihaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz B.,
                                                                                                                                                                                                                                В.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 445;
                                                                                                                                                                                                           TISSUE-Brain;
Minaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz
Minaylova-Todorova S.T., Choe S.M., Miller L.J., Horowitz
Westfall D.D.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY149906; AAN72326.1; --
EMBL; AY149906; AAN72326.1; --
EMBL; PRUB906; AAN72326.1; --
EMBL; PRUB906; AAN72326.1; --
EMBL; PRUB906; AAN72326.1; --
Interpro. IPR00407; GDAL_CD39_INPase.
Pfam; PRO1150; GDAL_CD39_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae,
                                                                                                                                                                                                                                                                                                                                                                                              445 AA; 48357 MW; 890CEFD068405698 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445
                                                                                                                                                                                                                                                                                                                                                                                                                                     82.2%; Score 1943; DB 2;
82.9%; Pred. No. 1.4e-144;
iive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 82.9
Matches 377; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10141;
                                                                                                                                                                                            FROM N.A.
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AAN72326;
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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AAN72326
ID AAN72326
DT 02-M
DT 02-M
DT 02-M
DT 02-M
DC 02-M
DC 02-M
DE 02-M

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171
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                                                                                                                                                                                                                                                                                                                       1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60
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MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Blosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane B.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
"Sequencing of an ectonucleoside triphosphate diphosphohydrolase homolog of NTPDase6 from guinea pig."; submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                          Length
                                                                                                                                           48357 MW; 890CEFD068405698 CRC64
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 6.
                                                                                                                                                                                                    82.2%; Score 1943; DB 2;
82.9%; Pred. No. 1.4e-144;
iive 31; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                       EMBL; AY149906; AAN72326.1;
                                                                                                                                                                                                                                                                    Matches 377; Conservative
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PRT;
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                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 53.2%
Matches 207; Conservative
                                                                                                                                 and mouse cDNA sequences.
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                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                         TISSUE=Prostate;
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                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                   Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAFGARWGQQAH
                                                                                                                                                                                                                                                                                                                                                                                          1 MRKIPNHGTLRMTKVAYPLGLCVGLFIYVAYIKWHRASAAQAFFTIAGAASGARWIQQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                               DB 2; Length 278;
                                                                                                                                                                                                                                                                                               52.0%; Score 1229.5; DB 2; Lengua
85.6%; Pred. No. 1.4e-88;
"Mismatches 18; Indels
                                                                                                                                                                    Strausberg R , Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                 278 AA; 30130 MW; 75A92DDIAC76297F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 5.
Name=EBtpd5;
                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272
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                                                                                                                                                                                            EMBL, BC038126, AAH38126.1; ...

MGD; MGI:1202295; Entpd6.

GC0:016787; F:hydrolase activity; IEA.

InterPro; IPR000407; GDA1_CD39_NTPase.

Pfam; PF01150; GDA1_CD39; 1.
                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J, TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Prostate;
MEDLINE=22388257; PubMed=12477932;
                                                                                                and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 237; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                  Query Mac.
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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EMBL; BC062044; AAHC044.1; --
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR00407; GDAI_CD39_NTPase.
Ffam; PF01150; GDAI_CD39; 1.
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, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus

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Chadwick B.P., Williamson J., Sheer D., Frischauf A.-M.; "CDNA cloning and chromosomal mapping of a mouse gene with homology to
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99298181; PubMed=10369669;
                                                                                                                                                                                   MEDLINE=98119025; PubMed=9457681;
                                                                                                                                                                                                                                                                                                Mamm. Genome 9:162-164(1998)
            Eukaryota; Metazoa;
                                                                                                                            SEQUENCE FROM N.A.
                                                         NCBI_TaxID=10090;
                                                                                                                                                           rissue=Testis;
                                          Mammalia;
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         RANGE COCCUCATE CONTRACTOR CONTRA
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F., Diatchenco L., Marusina K.P. Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodrigues A.C., Grimwood J., Schuutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., J. Marra M.A.; T. "Generation and initial analysis of more than 15,000 full-length human mannance of the control of the co
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53.2%; Pred. No. 6.9e-72;
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases
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Hydrolase.
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207; Conservative
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NEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;

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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                  PERCURNICE FROW N.A.

STRAIN-C57BL/64. TISSUBE-Kidney;

X GYRAIN-C57BL/64. TISSUBE-Kidney;

X DEDINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

A DAGAZAKI Y. Puruno M., Rasukawa T., Adachi J., Bono H., Kondo S.,

X Mikaido II., Osato N., Saito R., Suzuki H., Yamanaka II., Kiyosawa H.,

X Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

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X Baldarelli R., Hill D.P., Bult C., Corbani L.E., Cousins S.,

X Balla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

X Balla E., Dragani T.A., Fletcher C.F., Forrest A., Gugh J.,

R Basserland T., Garibold M., Gissi C., Godzik A., Gugh J.,

R Gasterland T., Garibold M., Gissi C., Godzik A., Gugh J.,

R Kanaj A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

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R Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

R Sandelin A., Schneider C., Semple C.A., Setcou M., Shimada K.,

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K Hara A., Hashizume W., Imotani K., Ishinagawa T., Ruduka S.,

K Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

K Yasunishi A., Yoshino M.,

K Yasaki Y., Barai K., Shinagawa T., Ruduka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is of the mouse transcriptome based on functional annotation of full-length cDNAs.",
Trombetta E.S., Helenius A.; "Glycoprotein reglucosylation and nucleotide sugar utilization in the secretory pathway: identification of a nucleoside diphosphatase in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                     endoplasmic reticulum.";
EMBO J. 18:3282-3292(1999).
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O9WUZ9; O70214; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Ectonucleoside triphosphate diphospholydrolase 5 precursor (EC 3.6.1.6) (WIPDase5) (Nucleoside diphosphatase) (CD39 antigen-like 4) (ER-UDPase).

Name=Entpd5; Synonyms=Cd3914; Mus musculus (Mouse).

427 AA

STANDARD;

ENPS MOUSE

MOUSE

7

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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Entpd5;
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                                                                                                                                                                                                                                                                                   08CD29
                                                                                                                                                                                                                                         RESULT 10
Q8CD29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNQEGEM 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 ATATQAFFSITRAAPGA-----RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGTLLQLTKKVNNIETGWALGATFHLLQSLGITS -> ERH
PLTAHKESEQHRDWLGLGGHLSPAPVSGHHQLRPSSTSEAC
                                                                            FUNCTION: Likely to promote reglycosylation reactions involved in glycoproteins folding and quality control in the endoplasmic reticulum. Hydrolyzes UDP, GDP and IDP but not any other nucleoside di-, mono- or triphosphates, nor thiamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISEPVFSQEGVDSETFSDLSGKAWPETR (in Ref. 1)
2F9DA2C342C55577 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEGM: PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39 NTPASE; FALSE NEG.
Calcium; Endoplasmic reticulum; Glycoprotein; Hydrolase; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F -> L (in Ref. 1).
DGTLLQLTKKVNNIETGWALGATFHLLQSLGITS
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                                                                                                                                                                   pyrophosphate.
CATALYIC ACTIVITY: A nucleoside diphosphate + H(2)0 = a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 1007; DB 1; Length 427;
; Pred. No. 8.8e-71;
62; Mismatches 133; Indels 10
                                                                                                                                                                                                                                                                                         PTM: N-glycosylated, high-mannose type.
MISCELLANEOUS: Optimal pH is neutral.
SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ectonucleoside triphosphate
                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
TISSUE SPECIFICITY: Ubiquitous.
                                                             U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diphosphohydrolase 5.
                                                                                                                                                                                                                                 COFACTOR: Requires calcium and magnesium
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EMBL, AJ238636; CAB45533.1; -.
EMBL, AK002618; BAB22234.1; -.
EMBL, BC015247, AAH15247.1; -.
MGD, MGI:1321385; Entpd5.
InterPro; IPR000407; GDA1 CD39 NTPase.
PF01150; GDA1 CD39; 1.
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                                                                                                                                                                                                             nucleotide + phosphate.
                                       and mouse cDNA sequences.
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Matches 213; Conservative
                                                             Sci.
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390
427
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SIGNAL 18
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                                                             Proc. Natl. Acad.
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390
394
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298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357
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MEDLINE=20499374; PubMed=11042L19;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
                                                                            384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGALF
                                                                                                                          PERAIN-C57BL/60; TISSUE-Pestis; MEDLINE-20530913; PubMed=11076861; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carminci P., Schono H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., "KIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embryo male testis CDNA, RIKEN full-length
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Genome Res. 10:1757-1771(2000)
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MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 AA.
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MEDLINE=21085660; PubMed=11217851;
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MEDLINE=99437879; PubMed=10506756;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 203
                                                                                                                                                                                                                                                                                                                                                             ATSWGAVFMLITACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58
         Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Harakida K., Hayatsu N., Hirawoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohato N., Okato N., Okazaki Y., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Soqabbe Y., Tagami M., Tagama A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasuushi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) Lo the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                            37 ATATQAFFSITRAAPGA-----RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG
                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                   ; Score 1007; DB 2; Length 427; ; Pred. No. 8.8e-71; 62; Mismatches 133; Indels 18
                                                                                                                                                                                                                                                              6E3773C842B58477 CRC64;
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Last annotation update)
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MGD; MGI:1321385; Entpd5.
GO; GO:0016787; F:hydrolase activity; IEA.
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Pfam; PF01150; GDA1_CD39; 1.
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    STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                              427 AA; 47101 MW;
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                                                                                                                                                                                                                                                                                         42.6%;
                                                                                                                                                                                                                                                                                                     Local Similarity 50.0
hes 213; Conservative
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DT 02-M

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STRAIN=CS7BL/G1 TISSUE=Bone;
MPDILINE=22354683;
The FANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Sukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
Recio J.A., Zambrano N., de La Pena L., Powers C., Siwarski D., Huppi K., Notario V.; "cDNA isolation, expression, and chromosomal localization of the ipph protro-oncogene."; Mol. Carcinog. 26:130-136(1999).

EMBL, AF136571; AAK82949.1; -. SEQUENCE 427 AA; 47101 MW; ZF9DA2C342C55577 CRC64;
                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                        Length 427;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male bone CDNA, RIKEN full-length enriched library,
clone: 9830144N04 product:ectomucleoside triphosphate
diphosphohydrolase 5, full insert sequence.
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                     ch 42.6%; Score 1007; DB 2; 3 il Similarity 50.0%; Pred. No. 8.8e-71; 213; Conservative 62; Mismatches 133;
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STRAIN-C57BL/6J; TISSUE=Bone;
MEDLINE=21085660; PubMed=11217851;
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298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 357
       the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE-Thymus; MEDILMB=20499374; PubMed=11042159; MEDILMB=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Mubkraction of cap-trapper-selected cDMAs to prepare full-length cDMA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                  324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA
                                                                                                                                                                               384 AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF
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MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsuninco H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
16 days neonate thywns cDNA, RIKEN full-length enriched library,
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymoll. 303:19-44(1999).
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MEDLINE=22354683; PubMed=12466851;
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MEDLINE=21085660; PubMed=11217851;
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Adachi J., Aizawa K., Airuno M., Hanagaki T., Hiraka T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiraka T., Hirozane T., Hori F., Indtani Y., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kadoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Chno M., Ohsato N., Okazaki Y., Nishi K., Nishi K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Towaru A., Toya T., Yasuku-Akahira S., Takeda Y., Tanaka T., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

BEMBI, AK036641; BAC29515.1; -.
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MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Hatemai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                         Shibata K., Itoh
                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizati Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
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                                                                                                                   STRAIN=C57BL/6J; TISSUE=Bone;
MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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213; Conservative
RIKEN FANTOM Consortium;
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STRAIN=CS'BEL/6J; TISSUE-Urinary bladder;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length COMS.";
                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Urinary bladder;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
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STRAIN=C57BL/6J; TISSUE=Thymus;
Adachi J., Aizawa K., Akimura;
Adachi J., Aizawa K., Akimura;
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hayashida K., Hangaki T., Hara A., Hashizume W.,
A Hori F., Indtani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato N.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Tushika H., Asunishi A., Muramatsu M., Hayashizaki Y.,
Bubmitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFLIGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 HSYLGFGLKAARLATLGALBAK-GTDGHTFRSACLPRWLBABWIFGGVKYQYGGNQEGEM
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14-APR-2004 (TrEMBLEE]. 27, Last annotation update)
Adult male urinary bladder CDNA, RIKEN full-length enriched library,
clone:9530068Al7 product-sectomodleoside triphosphate
diphosphohydrolase 5, full insert sequence.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;
                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                42.6%; Score 1007; DB 2; Length 427; 50.0%; Pred. No. 8.8e-71; ive 62; Mismatches 133; Indels 18
sequencing pipeline with 384 multicapillary sequencer."; eformet fes. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                 Matches 213;
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BA37592
ID BAC37
AC BAC37
AC BAC37
DT 14-AE
DT 14-AE
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AISWGAVFMLIIACVGSTVFYREQQTWFEGVFLSSMCPINVSAG---TFYGIMFDAGSTG 58
                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Urinary bladder;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoco R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawi J., RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachi, J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu W., Hiramoto K., Hiracoka T., Hirozama T., Hori F., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S. Kurihara C., Mateuryama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohazo N., Salto R., Salto H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami Promaru A., Toya T., Yakunishi A., Muramatsu M., Hayashizki Y., Tanaku T., Yabahitted (Apr. 2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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50.0%; Pred. No. 8.8e-71;
ive 62; Mismatches 133; Indels
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STRAIN=CS7BL/6J; TISSUB=Urinary bladder; MBDLINE=9279253; PubMed=10349636; Carninoi P., Hayashizaki Y.; High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Urinary bladder;
                                                                                                                                                               Meth. Enzymol. 303:19-44(1999)
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"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). RIKEN FANTOM Consortium; SEQUENCE FROM N.A.

STRAIN=CS7BL/67; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; "High-efficiency full-length, CDNA cloning."; Meth. Enzymol. 303:19-44(1999).

STRAIN=CS7BL/6J; TISSUB=Thymus;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to SEQUENCE FROM N.A.

Carrain-Carrain M., Akimura T., Arakawa T., Bono H., Carninci P., Rudda S., Purnon M., Hanagaki T., Hara A., Hashizume W., Pukuda S., Purnon M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Taqami M., A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (ARR-2002) to the BMBL/GenBank/DDBJ databases. genes."; STRAIN-C57BL/60; TISSUE-Thymus;
MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagooka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagooka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Warchiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-184-format Bequencing pipeline with 384 multicapillary sequencer."; new οĘ prepare full-length cDNA libraries for rapid discovery Genome Res. 10:1617-1630(2000). 427 AA; 47101 MW; 2F9DA2C342C55577 CRC64; Genome Res. 10:1757-1771(2000). EMBL; AK080265; BAC37862.1; SEQUENCE FROM N.A. SEQUENCE FROM N.A Hydrolase. SEQUENCE RTH REPRESENT SERVING SOLUTION SOLUTION SERVING SOLUTION SOLUTION SERVING SOLUTION S

9 263 323 383 58 TRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 204 INFLIGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS 324 LHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 37 ATATQAFFSITRAAPGA-----RWGQ----QAHSPLGTAADGHEVFYGIMFDAGSTG 264 YSYLGLGIMSARLAILGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 298 GFEPCYAEVLRVVQGKLHQPEEVRGSAFYAFSYYYDRAADTHLIDYEKGGVLKVEDFERK 358 AREVCDNLGSFSSGSPFLCMDLTXITALLKDGFGFADGTLLQLTKKVNNIETGWALGATF WKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT 239 HSYLGFGLKAARLATLGALEAK-GTDGHTFRSACLPRWLEAEWIFGGVKYQYGGNOEGEM 384 AKYVCRILETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF 18; Gaps Indels 62; Mismatches 133; DB 2; 42.6%; Score 1007; DB 2; 50.0%; Pred. No. 8.8e-71; Query Match
Best Local Similarity 50.09
Matches 213; Conservative 85 g à 8 g ð 요 셤 g à à d 8 ð

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Search completed: November 16, 2004, 16:59:41

Job time : 201 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 16, 2004, 16:32:53 ; Search time 156 Seconds (without alignments) 1048.593 Million cell updates/sec

US-09-905-589A-2

Perfect score: Title:

2364 1 MRKISNHGSLRVAKVAYPLG.....ALGAIFHYIDSLNRQKSPAS 456 Sequence:

BLOSUM62 Scoring table:

2002273 seqs, 358729299 residues Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:* A_Geneseq_23Sep04:*
1: __geneseqp1900s:*
2: __geneseqp1900s:*
3: __geneseqp2000s:*
4: __geneseqp2001s:*
5: __geneseqp2003s:*
6: __geneseqp2003ss:*
7: __geneseqp2003ss:*
8: __geneseqp2003ss:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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Result No.	Score	Query	Length	DB	ID	Description
	2364	100.0	456	- 5	AAE19881	CONTRACTOR DESCRIPTION OF THE PROPERTY OF THE
7	2364	100.0	456	8	AD099442	
ε.	2364	100.0	484	4	AAB72241	Himan
4	2364	100.0	484	œ	ADQ99473	Human
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9	2361	6.66	467	Ŋ	ABJ04657	7 Protei
7	2351	U١	456	4	AAM93929	6
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σ	2152	91.0	450	7	ADC14220	Human
10	2135	90.3	462	4	AAU30882	Norrel
11	2116	89.5	446	ß	ABJ04658	B Drotei
12	2003	84.7	471	4	AAB72242	
13	666	42.3	428	3	AAY44849	ıσ
14	666	42.3	428	4	AAB72238	Human
15	666	42.3	428	4	AAB72243	3 Himan
16	666	42.3	428	S	AAE19883	3 Human
17	666	42.3	428	ω	ADP07487	Human
18	666	42.3	428	æ	ADP07485	
61	666	42.3	428	æ	ADQ99446	Human
20	666	42.3	428	œ	ADQ99449	Human
21	966	42.1	428	m	AAY44850	Human
22	966	42.1	428	4	AAB72240	Himan 0
23	992	42.0	428	7	ADJ70490	uemil 0
24	992	42.0	428	œ	ADP07489	Human
25	606	38.5	405	6	AAY44851	Human

Aab72239 Himan Ch3					Droson											Toxic			
AAB72239	ADP07491	AAE19884	ADQ99448	AAB53336	ABB66213	ADQ99472	ABB59611	AAU30879	AAU30881	AAW85687	AAW85684	AAU78818	AAW85685	AAU78819	ADK36500	AD060417	ABP81286	ABM74049	ADJ57264
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38.5	38.5	38.2	38.2	34.8	26.3	26.3	26.3	25.2	25.2	21.9	21.4	21.4	21.2	21.2	20.9	20.7	20.7	20.6	20.5
606	606	904	904	823	621	621	621	296	296	518.5	206	206	501	501	495	490	488.5	486	485
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAE19881 standard; protein; 456 AA. AAE19881

AAE19881;

(first entry) 18-JUN-2002

Human CD39L2 protein.

Human; CD-39-like protein; CD39L2 protein; therapy; immune deficiency; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis, autoimmune thyroiditis; allergic reaction; asthma; insulin dependent diabetes mellitus; periodontal disease, osteoporosis; osteoarthritis; wound healing; tissue repair; Alzheimer's disease; ulcer; Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease; nervous system disease; nerve injury; ischaemia-reperfusion injury; nerve injury; ischaemia-reperfusion injury; condotoxin lethality; arthritis; nephritis; inflammatory bowel disease; Crohn's disease; Crohn's disease; virucide; antibacterial; antifungal; neuroprotective; dermatological; immunosuppressive; vulnerary; nootropic; anticonvulsant; antiinflammatory; nephrotropic; gastrointestinal; vasotropic.

Homo sapiens

US6350447-B1.

26-FEB-2002.

99US-00240639. 29-JAN-1999; 99US-00240639. 29-JAN-1999;

(HYSE-) HYSEQ INC.

WPI; 2002-215262/27.

Chadwick BP, Frischauf A;

N-PSDB; AAD31693

An isolated polypeptide with phosphohydrolase activity, designated CD39L2, useful to identify other proteins with which binding occurs or identify inhibitors and for treatment of, e.g., Alzheimer's, multiple sclerosis and osteoporosis.

Claim 1; Fig 4; 101pp; English.

The present invention relates to novel proteins with phosphohydrolase activity, designated CD-39-like (CD39L) proteins and polymucleotides

23-SEP-2004 (first entry)

conditions such proteins are useful to treat interction that may diseases caused by viral, bacterial, fungal or other infection that may be treatable with CD30. They are useful in the treatment of various immune deficiencies and disorders, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune thyroiditis and insulin dependent diabetes mellitus, allergic reactions thyroiditis and insulin dependent diabetes mellitus, allergic reactions and conditions such as asthma and other respiratory problems, periodontal disease, osteoporosis, osteoarthritis and other tooth repair processes. They may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration as well as for wound chealing and tissue repair and replacement and in the treatment of burns, incisions and ulcers. CD30 proteins may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central nervous system diseases such as Alzheiner's disease, parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, parkinson's disease, amyotrophic lateral sclerosis, Huntington's creat mechanical and traumatic disorders witch involve degeneration, creat mechanical and traumatic disorders witch involve degeneration, cheating wounds including pressure ulcers witch involve degeneration, vascular insufficiency and surgical and traumatic wounds. They also exhibit anti-inflammatory activity and may be used to treat inflammatory activity and may be used to treat inflammatory expectation or acute conditions), including presente conditions), including ischemial crepticion injury, endotoxin lethality, arthritis, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease or Crohn's disease. The present sequence is human CD3912 protein CD39L proteins are useful to treat infectious . 0 100.0%; Score 2364; DB 5; Length 456; 100.0%; Pred. No. 1.2e-215; ive 0; Mismatches 0; Indels 0 Matches 456; Conservative such proteins. Best Local Similarity Sequence 456 AA; 61 61 121 181 181 241 301 Query Match \$

ö 240 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420 120 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT 240 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 LQASPPGYLTALRMENRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 9 9 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD **VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP** FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 456 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456 KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 361 421 421 ð qq 8 g qq à qq g ð ò g à

121 VEKSAQGIRELLDVAKQDIPPDFWKATPLVLKATAGIRLLPGEKAQKLLQKVKEVFKASP 180

61

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ADQ99442 standard; protein; 456 AA

RESULT 2 ADQ99442

ADQ99442;

EXXX.

09 9

The invention relates to novel CD39-like polypeptides (CD39-like nucleotide triphosphatase, NTPase) and nucleic acid molecules encoding such polypeptides. CD39-like polymucleotides may be used as hybridisation probes, PCR primers and in chromosome and gene mapping. Polypeptides of the invention may be used as molecular weight markers, as food supplements, in generating an antibody that specifically binds the solypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or for regulating ATP neurotransmission in smooth muscle, peripheral ganglia or brain. Sequences of the invention are useful in modulating ecto-ATPase activity and for identifying compounds that modulate ecto-ATPase activity. The present sequence is human CD39-like protein, CD39L2. Note: This sequence is stated to be the same as that shown in Figures 8 and 9, however the sequence is truncated at it's N-terminal. The longer sequence is represented in ADQ99473. SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 CD39-like protein; gene mapping; molecular weight marker; food supplement; anti-thrombotic; anti-tissue graft rejection agent; ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase; 1 MRKISNHGSLRVAKVAYPLGLCVGVF1YVAYIKWHRATATQAFFSITRAAPGARWGQQAH 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH New CD-39-like polypeptides and polynucleotides, useful in chromosome gene mapping, as molecular weight markers, as food supplements, or as anti-thrombotic or anti-tissue graft rejection agents. Gaps ., 100.0%; Score 2364; DB 8; Length 456; 100.0%; Pred. No. 1.2e-215; ive 0; Mismatches 0; Indels 0; TII "II ľΔ H /note= "Apyrase region (ACR) /note= "Apyrase region (ACR) "Apyrase region region Claim 2; SEQ ID NO 2; 104pp; English cocation/Qualifiers /note= "Apyrase Human CD39-like protein, CD39L2 99US-00240639 13-JUL-2001; 2001US-00908510 Chadwick BP, Frischauf A; .239 .266 Matches 456; Conservative /note= NTPase; human; enzyme. WPI; 2004-515395/49. Local Similarity (NUVE-) NUVELO INC Sequence 456 AA; N-PSDB; ADQ99441 29-JAN-1999; Homo sapiens. US6759214-B1 Query Match Region Region Region Region g ä

and

cerebral

arterial thrombosis,

cerebral ischaemia, angina,

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artery thrombosis or intracardiac thrombosis, and conditions associated with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in modulating disease states (including platelet aggregation, inflammation and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPs. The polypeptides are also useful for prophylaxis or treatment of inflammation related disorders, such as disorders involving sepsis or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea, cytokine overstimulation); autoimmune disorders such as thrombosis, cytokine overstimulation); autoimmune disorders including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents human CD39 like protein CD39-L2

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Sequence 484 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CD39-like protein, apyrase, NDPase, platelet function inhibitor, myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis, platelet aggregation; inflammation, apoptosis, autoimmune disorder, neurological disorder;
                                                        FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                                                                                                                                                                                    241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                                  LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                                                                                                                                                                                                                                                                          AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease; Parkinson's disease; cancer; CD39-L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CD39 like protein CD39-L2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
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11-JAN-2000; 2000US-00481238.
25-APR-2000; 2000US-00557800.
25-MAX-2000; 2000US-00583331.
30-JUN-2000; 2000US-00608285.
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 448
 88
 food supplement; anti-thrombotic; anti-tissue graft rejection agent; ATP neurotransmission; ecto-ATPase activity; nucleotide triphosphatase;
 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
 89 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
 209 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
 61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
 269 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
 SFKGEWEHAEVTYRVSGOKAAASLHELCAARVSEVLONRVHRTEEVKHVDFYAFSYYYDL
 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
 329 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
 Gaps
 0;
 Length 484;
 CD39-like protein; gene mapping; molecular weight marker;
 Indels
 ; Score 2364; DB 4;
; Pred. No. 1.3e-215;
0; Mismatches 0;
 456
 421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS
 449 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS
 ADQ99473 standard; protein; 484
 Human CD39-like protein, CD39L2
100.0%;
 (first entry)
 Matches 456; Conservative
 NTPase; human; enzyme.
 Local Similarity
 23-SEP-2004
 181
 241
 Query Match
 301
 ADQ99473
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Homo sapiens

This invention relates to polynucleotides encoding human CD39-like polypeptides with apyrase and/or NDPase activity. The polypeptides having ATPDase, including NDPase, activity are useful for inhibiting platelet function and can therefore be used in the prophylaxis or treatment of pathological conditions caused by or involving thrombosis or excessive coagulation or excessive platelet aggregation, such as myocardial

Claim 39; Page 162-164; 203pp; English.

inflammatory disorders.

pathological and

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New CD-39-like polypeptides and polynucleotides, useful in chromosome and
 gene mapping, as molecular weight markers, as food supplements, or as anti-thrombotic or anti-tissue graft rejection agents.
 The invention relates to novel CD39-like polypeptides (CD39-like
 Claim 2; Fig 8A-D; 104pp; English.
 13-JUL-2001; 2001US-00908510
 N-PSDB; ADQ99441, ADQ99441.
 WPI; 2004-515395/49.
 (NUVE-) NUVELO INC
 Chadwick BP,
 29-JAN-1999;
US6759214-B1
 06-JUL-2004,
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nucleotide triphosphates, Nate 2017 Ann profession mucleotide triphosphates, Nate 2017 Ann profession probes, PCR primers and in chromosome and gene mapping. Polypeptides of probes, PCR primers and in chromosome and gene mapping. Polypeptides of the invention may be used as molecular weight markers, as food supplements, in generating an antibody that specifically binds the polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or for regulating ATP neurotransmission in smooth muscle, peripheral ganglia or brain. Sequences of the invention are useful in modulating ecto-ATPase activity and for identifying compounds that modulate ecto-ATPase activity. The present sequence is human CD39-like protein, CD3912. Note: This sequence is stated to be the same as that shown in SEQ ID 2 of the sequence listing, however this sequence is longer at the N-terminal. The shorter sequence is represented in ADQ99442. . 0 Length 484; Indels 100.0%; Score 2364; DB 8; 100.0%; Pred. No. 1.3e-215; . 0 0; Mismatches Query Match Best Local Similarity 100. Matches 456; Conservative Sequence 484 AA;

1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 60 Gaps

VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRILPGEKAQKLLQKVKEVFKASP 208 SFKGEWEHAEVIYRVSGQKAAASLHELCAARVSEVLQNRVHRIEEVKHVDFYAFSYYDL 388 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 SPKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328 29 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 88 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGTQIAFLPRVEGT 329 61 83 121 149 181 209 241 269 301 q g g q 쉽 8 ò à g ð 8

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ABB06124 standard; protein; 463 AA. ABB06124

(first entry) 10-MAY-2002

ABB06124;

99US-00240639

Frischauf A;

Human NS protein sequence SEQ ID NO:216.

Human; cytostatic; osteopathic; gynaecological; neuroprotective;

W antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;

KW antiarteriosolerotic; antiplanmatory; dermatological;

KW anorectic; muscular; antialteriosolerotic; antidepressular; anticoagulant;

W antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;

KW anticonvulsant; antidabetic; tranquilliser; antidepressant; aeuroleptic;

KW anticonvulsant; antidabetic; tranquilliser; antidepressant; aeuroleptic;

KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;

KW contraceptive; degenerative disease; multiple solerosis; pstonia;

KW rheumation; skin disease; multiple solerosis; glaucoma;

KW inflammation; skin disease; coagular dystrophy; AIDS;

KW inflammation; skin disease; coagulation disease; hypertension;

KW gastric ulcer; Alzheimer's disease; epilepsy; angina; neurodegeneration;

KW gastric ulcer; Alzheimer's disease.

Homo sapiens.

24-JAN-2002

17-JUL-2001; 2001WO-IL000653

18-JUL-2000; 2000IL-00137345 15-DEC-2000; 2000IL-00140354

(COMP-) COMPUGEN LTD.

Bernstein J; Mintz L, Freilich S,

WPI; 2002-155037/20. N-PSDB; ABL39778 One hundred and twenty eight novel nucleic acid sequences, useful for treating and diagnosing e.g. cancer, asthma and Alzheimer's.

Claim 6; Page 251-253; 290pp; English

ABL39691 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB06037 to ABB06164. The novel sequences (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective, antirheumatic, antiarthritic, antiphrancial cophinal mological, virucide, vasotropic, antiarthritic, antiinflammatory, dermafological, virucide, vasotropic, antiarteriosclerotic, antiinflammatory, dermafological, virucide, anticogniant, antifibinolytic, hypotension, antiasthmatic, cardiant, immunomodulator, antiiconvulsant, antidiabetic, tranquilliser, antiulcer, antidepressant, gastrointestinal, aeuroleptic, crebroprotective, cardiant, anticopic and contraceptive activities. The NS can be used in vaccines, gene therapy and antisense therapy. Nucleic acids, expression vectors and antibodies from the present invention can be used for treating and cantibodies from the present invention can be used for treating and disease, dysforia, multiple sclerosis, rheumatoid arthritis, psoriasis, cataracts, restenosis, atherosclerosis, inflammation, skin disorders, diseases, opsilation disease, ischaemia, hypertension, asthma, immune disease, achizophrenia, viral disease, gastric ulcers, stroke, depression, schizophrenia, viral disease, gastric ulcers, stroke, all contraceptive

Sequence 463 AA;

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o,
 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPCLSAYADD 120
 180
 240
 127
 187
 FLVGDDCVSIMNGTDEGVSAMITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLFRVEGT 247
 LOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
 9
 67
 8 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
 VEKSAQGIRELLDVAKQDI PFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKBVFKASP
 128 VEKSAGGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 Gaps
 .
0
 Length 463;
 0; Indels
99.9%; Score 2361; DB 5;
99.8%; Pred. No. 2.3e-215;
tive 1; Mismatches 0;
 KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
 455; Conservative
 Similarity
 61
 121
 Query Match
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 181
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ABJ04657 standard; protein; 467 ABJ04657; ABJ04657 ID ABJ( XX RESULT 

(first entry) 11-OCT-2002

Protein of NOVX 15a SEQ ID No 36,

Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic; neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective; tranquiliser; neuroleptic; antidabetic; antidate; antidatory; antidabetic; disorder; disorder; obesity; immune disorder; haematopoidic disorder; dasorder; neurological disorder; esplepsy; stroke; mental disorder; schizophrenic disorder; vesicular transport; cystic fibrosis; gastrointestinal disorder; diabetes mellitus; ulcerative colitis; AIDS; allergic reaction; multiple sclerosis; rheumatoid arthritis; transgenic animal;

gene therapy

Unidentified

06-DEC-2001; 2001WO-US046586

06-DEC-2000; 2000US-0251660P. 12-DEC-2000; 2000US-025529P. 08-JAN-2001; 2001US-0260326P.

2001US-0269942P. 2001US-0286183P. 2001US-0313627P. 2001US-0318712P. 20-FEB-2001; 24-APR-2001; 12-SEP-2001; 20-AUG-2001; 

(CURA-) CURAGEN CORP

Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM; Tchernev VT, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP; Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog Fl Colman SD, Elsen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;

WPI; 2002-547774/58. N-PSDB; ABT05470. Novel isolated polypeptide, designated NOVX, useful for treating opreventing cancer, diabetes, obesity, dyslipidemia, anorexia, and metabolic, neurodegenerative, immune and hematopoietic disorders.

Claim 1; Page 140; 421pp; English.

The invention relates to an isolated polypeptide, designated NoVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polymuclectide or an antibody created from the protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NoVX-associated disorder, or for treating or preventing a NOVX-associated disorder in a subject, preferably muman. The isolated protein, its encoding polymuclectide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorder, Alaheimer's disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with objunclectide or an antibody created from the protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, disorders including mood, anxiety, schizophrenic disorders.

Commutal disorders including mood, anxiety, schizophrenic disorders of vesicular transport such as cystic fibrosis, diabetes colitis, other conditions associated with abnormal vesicle trafficking conducing Albs, allergic reactions, multiple sclerosis and theumatonic arthering arthering an endication and any enveronment of the invention is useful for arthering and premarial for any enveronment of the invention is setting for any enveronment of the invention is setting for any enveronment of the invention is setting for any enveronment of the invention and any enveronment of the invention is nearly for any enveronment of the invention is setting for any enveronment of the invention is such as full for any enveronment of the invention is such as full for any enveronment of the invention is such as full for any enveronment of the enveron arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynuclectide of the invention can be used to treat disorders by gene therapy. This sequence represents one of the isolated NOVX proteins of the invention

Gaps .; 0 Length 467; Indels 99.9%; Score 2361; DB 5; 99.8%; Pred. No. 2.4e-215; iive 1; Mismatches 0; Query Match
Best Local Similarity 99.8°
Matches 455, Conservative

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121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180 191 d ð 임

240 251 181 FLVGDDCVSIMNGTDEGVSAWITINFLIGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT ð 쉽

241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 ð

Sequence 467 AA;

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SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
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 421
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 8
 The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length not form A of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in CD-ROM format directly from EPO
 Primers useful for synthesizing full length cDNA clones and their use
 420
 360
 431
 312 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYDL
 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
 Η,
 Kawai Y;
T, Koga
 Length 456;
 claim 8; SEQ ID NO 4100; 1380pp + Sequence Listing; English.
 Ishii S, I
S, Otsuki
 Human; full length cDNA; cDNA synthesis; oligo-capping
 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 467
 Score 2351; DB 4;
Pred. No. 2e-214;
1; Mismatches 2;
 Hayashi K, Is
K, Kojima S,
 AAM93929 standard; protein; 456 AA
 Human polypeptide, SEQ ID NO: 4100
 Nishikawa T, Isogai T,
su A, Sugiyama T, Nagai
 08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
 99.5%;
 07-JUL-2000; 2000EP-00114089.
 Wakamatsu A, Sugiyama T,
 (first entry
 genetic manipulation.
 (HELI-) HELIX RES INST.
 2001-524255/58.
 N-PSDB; AAK94892
 Sequence 456 AA;
 EP1130094-A2
 06-NOV-2001
 05-SEP-2001
 432
 361
 421
 AAM93929
 ota T,
 830
 RESULT
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/target molecules in the field of medicine, and in particular genes
 420
 300
 300
 360
 360
 420
61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHHTFKALKPGLSAYADD
 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATVGLRLLPGEKAQKLLQKVKEVFKASP
 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
 synthesizing full
 H
 human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method.
 Kawai Y;
 Human protein encoded by a full length cDNA clone SeqID 4100.
 Isogai T, Hayashi K, Ishii S, Kawa
Na T, Nagai K, Kojima S, Otsuki T,
 New oligonucleotide primers (830 cDNAs) useful for length human cDNAs.
 KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 Example 1; SEQ ID NO 4100; 1340pp; English
 Ā
 456
 (REAS-) RES ASSOC BIOTECHNOLOGY
 11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
 07-JUL-2000; 2003EP-00025638.
 99JP-00194486.
 ADL32067 standard; protein;
 Sugiyama T,
 (first entry)
 Nishikawa T,
 WPI; 2004-204755/20.
N-PSDB; ADL32066.
 Wakamatsu A,
 08-JUL-1999;
 EP1396543-A2
 10-MAR-2004
 20-MAY-2004
 ADL32067;
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.. 0

Gaps

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2; Indels

Best Local Similarica Matches 453; Conservative

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Query Match Best Local Similarity

9 09

1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATAIQAFFSITRAAPGARWGQQAH ^

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ö
 120
 120
 180
 240
 180
 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
 encoding proteins that are associated with Signal Commercial, a glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 LOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGOPAKDGKELVSPCLSP 300
 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
 9
 9
 61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKALKPGLSAYADD
 VEKSAQGIRELLDVAKQDI PFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATVGLRLLPGEKAQKLLQKVKEVFKASP
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 Gaps
 .,
0
 99.5%; Score 2351; DB 8; Length 456; 99.3%; Pred. No. 2e-214; ive 1; Mismatches 2; Indels
 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 al Similarity 99.3
453; Conservative
 AA;
 Sequence 456
 121
 Query Match
Best Local (
 181
 181
 241
 301
 361
 361
 421
 421
 301
 Matches
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enzyme; human; ENZM; cytostatic; antiarteriosclerotic; antidiabetic; anticonvulsant; nootropic; neuroprotective; cerebroprotective; antiallerapt; antiinflammatory; thyromimetic; gene therapy; cell proliferative disorder; endocrine disorder; neurological disorder; immune system disorder; inflammatory disorder; developmental disorder; reproductive disorder; reproductive disorder; reforder; disorder; disorder; sexicle-trafficking disorder; infection.
 Æ
 ADC14220 standard; protein; 450
 (first entry)
 Human enzyme ENZM-26.
 WO2003042357-A2
 sapiens
 18-DEC-2003
 ADC14220;
 Jomor
 ADC14220
RESULT
```

28-SEP-2001; 2001US-032638BP. 12-OCT-2001; 2001US-0328979P. 19-OCT-2001; 2001US-0346034P.

26-SEP-2002; 2002WO-US031096

268

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The invention relates to a novel isolated human enzyme (ENZM)

polypeptide. A polypeptide of the invention has cytostatic,
antiatreriosclerotic, antidiabetic, anticorvulsant, nootropic,
antiatreriosclerotic, antidiabetic, anti-HIV, antiallergic,
antinflammatory, and thyromimetic activity. A polynuclectide encoding a
polypeptide of the invention may have a use in gene therapy. The
polypeptide of the invention may have a use in gene therapy. The
polypeptide of the invention may have a use in gene therapy. The
polypeptide of the invention may have a use in gene therapy. The
polypeptide of the invention may have a use in gene therapy. The
polypeptide of the invention may have a use in denetherapy. The
polypeptide of the invention of ENZM, such as cell proliferative (e.g.
capression or overexpression of ENZM, such as cell proliferative (e.g.
cancer, atherosolerosis), endocrine (e.g. diabetes), neurological (e.g.
capcing), developmental (e.g. Hypothyroidism, Cushing's syndrome),
reproductive and vesicle-trafficking disorders, or infections. These are
also useful in assessing the effects of exogenous compounds on the
expression of nucleic acid and amino acid sequences of ENZM. The ENZM
its fragments are useful in screening compounds for effectiveness as
its fragments are useful in screening compounds that specifically bind to or
modulate the activity of the polypeptide. The microarray is useful in
modulate the activity of the polypeptide. The microarray is useful in
modulate interactions, and dene expression profiles. The microarray is useful in
theractions.
 120
 180
 208
 240
 New human enzymes (ENZM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant ENZM expression e.g.
 Yang J, Lu DAM, Yue H, Elliott VS, Warren BA, Duggan BM;
Forsythe IJ, Lee EA, Hafalia AJA, Ramkumar J, Chawla NK, Baughn MR
Becha SD, Gorvad AE, Tran UK, Li JX, Yao MG, Ison CH, Griffin JA,
Lee SY, Chang H, Emerling BM, Tang YT, Lal PG, Kable AE;
Marquis JP, Jiang X, Jackson AA, Zebarjadian Y, Swarnakar A,
Wilson AD, Jin P, Richardson TW, Bhatia U, Burrill JD, Lee S;
Blake JJ, Ho A, Zheng W, Gao J;
 Baughn MR;
 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGOOAH
 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT
 PLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 34; Gaps
 interactions, and gene expression profiles. The sequences shown ADC14195-ADC14247 represent ENZM proteins of the invention.
 Length 450;
 Indels
 91.0%; Score 2152; DB 7;
92.3%; Pred. No. 1.7e-195;
iive 1; Mismatches 0;
 cancer, diabetes, epilepsy, or infections.
 Claim 1; SEQ ID NO 26; 416pp; English.
 2001US-0338048P.
2001US-0332340P.
2001US-036772.
2002US-0368722P.
2002US-0368799P.
2002US-0381558P.
2002US-0381558P.
 (INCY-) INCYTE GENOMICS INC
 Matches 421; Conservative
 WPI; 2003-449567/42.
 Local Similarity
 N-PSDB; ADC14273.
 Sequence 450 AA;
26-OCT-2001;
08-NOV-2001;
16-NOV-2001;
 29-MAR-2002;
29-MAR-2002;
17-MAY-2002;
07-JUN-2002;
21-JUN-2002;
 14-DEC-2001;
 Query Match
 53
 19
 89
 121
 149
 181
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The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used to express them are also useful for producing the proteins. The proteins and/or nerve tissue growth or regeneration; immune suppression and/or and/or nerve tissue growth or regeneration; immune suppression and/or setzited proteins of the invention acid sequences of novel human acceptance.
 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRILETQPQSSPFSCMDLTVVSLLLQEFGFPRS 414
LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
 301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
 Human, vaccination, gene therapy, nutritional supplement,
stem cell proliferation, haematopoiesis, nerve tissue regeneration,
immune suppression; immune stimulation, anti-inflammatory; leukaemia.
 LOASPPGYLTALRMFNRTYXLYSYSYLGLGLMSARLAILGGVEGQP-
 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 450
 Claim 20; Page 365; 765pp; English.
 Novel human secreted protein #1373.
 ΑĀ
 AAU30882 standard; protein; 462
 16-APR-2001; 2001WO-US008656
 18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
 entry)
 (first
 WPI; 2001-611725/70.
 (HYSE-) HYSEQ INC.
 Liu C,
 WO200179449-A2.
 25-OCT-2001.
 18-DEC-2001
 Tang YT,
 421
 AAU30882;
 315
 355
 415
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 Homo
 AAU30882
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300

244

304

245 LQASPPRYLTALRMFNRTYKLYCXSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP

241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP

VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180

SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQF--

125 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP

FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT 185 FLVGDDCVSIMNGTNEGVSAMITINFLTGSLKTPRRSNVGMLDLGGGSTQIVFLTHVEGT

181

g

SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120

MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRANATQAFFSITRAAPGARWGQQAH

29 61 89 121

ò 셤 à q à g ò

1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH

184 240

------XADD 124

88

Gaps

26;

Length 462; Indels

Score 2135; DB 4; Pred. No. 7.5e-194;

90.3%; 92.1%;

Query Match 90.3 Best Local Similarity 92.1 Matches 422, Conservative

2; Mismatches

360

364 418

SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL

305

d

à

ò g à

301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL

365 AAGVGLIDAEKGGSLVVGDFEIAAKYVCVRTLGETQPQSSPFSCMDLTYVSLLLQEFGFP 424

d à

419 RSKVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456

361 AAGVGLIDAEKGGSLVVGDFEIAAKYVC-RTL-ETQPQSSPFSCMDLTYVSLLLQEFGFP

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neuroprotective; anniparkinsontan; anticonvulsant; cerebroprotective; tranquiliser; neuroleptic; antidabetic; anticonvulsant; cerebroprotective; tranquiliser; neuroleptic; antidabetic; antialter; outiinflammatory; metabolic disorder; obesity; infectious disease; Alzheimer's disease; anorexia; neurodegenerative disorder; Parkinson's disorder; obesity; metabolic syndrome X; wasting disorder; dyslipidaemia; chronic disease; epilepsy; stroke; mental disorder; cancer; neurological disorder; epilepsy; stroke; mental disorder; schizophrenic disorder; goiter; diabetes mellitus; ulcerative colitis; AlDS; allergic reaction; multiple sclerosis; rheumatoid arthritis; transgenic animal;
 Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic;
425 RSKVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 462
 Protein of NOVX 15b SEQ ID No 38.
 ABJ04658 standard; protein; 446
 06-DEC-2000; 2000US-0251660P.
12-DEC-2000; 2000US-0255029P.
08-JAN-2001; 2001US-0260326P.
 06-DEC-2001; 2001WO-US046586
 Unidentified.
 gene therapy
 11-OCT-2002
 13-JUN-2002
 ABJ04658;
 RESULT 11
 ABJ04658
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Sequence 462 AA;

σ

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L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM;
T, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP;
Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog Fl
Eisen AJ, Liu X, Padigaru M, Spaderna SK, Zerhusen BD;
 20-FEB-2001; 2001US-0269942P.
24-APR-2001; 2001US-02861B3P.
20-AUG-2001; 2001US-0313627P.
2001US-0263800P
 2001US-0318712P
 (CURA-) CURAGEN CORP
 WPI; 2002-547774/58.
 N-PSDB; ABT05471
 Guo X, Li L,
Tchernev VT,
Edinger S, P
 12-SEP-2001;
 Colman SD,
```

Novel isolated polypeptide, designated NOVX, useful for treating opreventing cancer, diabetes, obesity, dyslipidemia, anorexia, and metabolic, neurodegenerative, immune and hematopoietic disorders. Claim 1; Page 141; 421pp; English.

The invention relates to an isolated polypeptide, designated Novx, comprising a sequence fully defined in the specification. The isolated protein, its encoding polymucleotide or an antibody created from the protein is useful in the manufacture of a medicament for treating a disorder. For the control of preventing a NOVX-associated disorder in a subject, preferably human. The isolated protein, its encoding usubject, preferably human. The isolated protein, its encoding of subject, preferably human. The isolated protein, its encoding of polymucleotide or an antibody created from the protein are also useful for treating or preventing metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorder, harbeimer's disorder, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome. X, wasting disorders associated with obesity, the metabolic syndrome X, wasting disorders associated with obsity, the metabolic syndrome X, wasting disorders associated with obsity, the metabolic syndrome X, wasting disorders associated from the protein are useful for treating or preventing neurological disorders such as epilepsy, stroke, mental disorders including underological disorders including ulcerative colities, other conditions associated with abnormal vesicle trafficing including AIDS, allergic reactions, multiple sclerosis and rheumatoid arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polynucleotide of the invention can be used to treat disorders by gene therapy. This sequence represents one of the isolated NoVX proteins of the invention

Sequence 446 AA;

SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 29 MRKISNHGSLRVAV-----ARWGQQAH 50 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 231 LOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKGVFKASP FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 38; Gaps 89.5%; Score 2116; DB 5; Length 446; 91.0%; Pred. No. 4.6e-192; 2; Indels 1; Mismatches Local Similarity 91.0 Les 415; Conservative 51 171 61 181 Query Match Matches Пb 임 d ò 음 à à ð ð

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This invention relates to polynucleotides encoding human CD39-like polypeptides with apyrase and/or NDPase activity. The polypeptides having propypetides with apyrase and/or NDPase activity. The polypeptides having ATPDAse, including NDPase, activity are useful for inhibiting platelet function and can therefore be used in the prophylaxis or treatment of pathological conditions caused by or involving thrombosis or excessive coagulation or excessive platelet aggregation, such as myocardial infarction, cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis or intracardiac thrombosis, and conditions associated with venous thrombosis. CD39-LL4 and CD39-LL2 polypeptides are useful in modulating disease states (including platelet aggregation, inflammation and apoptosis) associated with ADP or other purinergic signalling by reducing the levels of NDPs. The polypeptides are also useful for prophylaxis or treatment of inflammation related disorders, such as prophylaxis or treatment of inflammation related disorders, such as classification or systemic inflammatory response syndrome or SIRS (and associated conditions such as fever, tachycardia, tachypnea,
 410
 Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDPase activity, which are useful in the treatment of pathological conditions caused by thrombosis (e.g. myocardial infarction) and
 thrombosis;
 Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
 351 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGPPRS
 291 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
 myocardial infarction, cerebral ischaemia, angina, arterial throcerebral artery thrombosis, platelet aggregation, inflammation, apoptosis, autoimmune disorder, neurological disorder,
 Mature human CD39 like protein CD39-L2 amino acid sequence.
 Alzheimer's disease; Parkinson's disease; cancer; CD39-L2.
 411 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 446
 421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
 Claim 53; Page 192-194; 203pp; English.
 AAB72242 standard; protein; 471
 2000US-00481238.
2000US-00557800.
2000US-00583231.
2000US-00608285.
 Yeung G;
 09-AUG-2000; 2000WO-US021790.
 99US-00370265.
 14-MAY-2001 (first entry)
 inflammatory disorders.
 Mulero JJ,
 WPI; 2001-147489/15
 (HYSE-) HYSEQ INC.
 N-PSDB; AAF63387
 WO200110205-A1.
 09-AUG-1999;
 Homo sapiens
 11-JAN-2000;
 25-APR-2000;
26-MAY-2000;
 30-JUN-2000;
 15-FEB-2001
 AAB72242;
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 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 148
 240
 300
 328
 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 388
 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120
 VEKSAQGIRELLDVAKQDIPPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
 88
 CD39-L4; human, apyrase; nucleotide diphosphatase; NDPase; ATP Diphosphohydrolase; ATPDase; adenosine diphosphate; ADP; treatment; platelet aggregation; antithrombotic; thrombosis; myocardial infarction; cerebral ischaemia; angina; vascular graft; extracorporeal circulation; molecular weight marker; nutritional supplement; tumour; prevention; drug targeting; Apyrase Conserved Region; ACR.
 atherosclerosis, acute pancreatitis, dermatitis, including psoriasis, cirrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis; neurological disorders including neurodegenerative diseases, epilepsy, depression, Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis; and cancer. The present sequence represents mature D39 like protein CD39-L2
 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
 VEKSAQGIRELLDVAKQDIPPDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
 LOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYDL
 MKKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT
 Gaps
overstimulation); autoimmune disorders such as thrombosis
 0
 CD39"
 Length 471;
 Indels
 murine
 /label= Mature_human_CD39-L4_protein
/note= "Homologous to human and murir
 Score 2003; DB 4; L
Pred. No. 2.8e-181;
1: Mismatches 5;
 AAGVGLIDAEKGGSLVVGDFEIAAKYGGSHLERE 422
 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQ 394
 'label= ATP_Binding_region
 1; Mismatches
 1. .22
/label= Leader_peptide
 Socation/Qualifiers
 Ā
 428
 84.7%;
 AAY44849 standard; protein;
 (first entry)
 .428
 Conservative
 58
 Human CD39-L4 protein.
 Similarity
 Sequence 471 AA;
 Binding-site
 Homo sapiens
 18-MAY-2000
 388;
 389
 209
 AAY44849
 29
 61
 121
 149
 181
 241
 269
 329
 361
 Query Match
 301
 Peptide
 Protein
 Local
 Region
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 Matches
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The present amino acid sequence is the CD39-L4 protein, an apyrase and/or nucleotide diphosphatase (NDPase). It is isolated from the human foetal liver-splean cDNA library, b2HFLS20W. It is a soluble ATP Diphosphohydrolases (ATPDase) and is involved in the hydrolysis of adenosine diphosphate (ADP), the agonist that causes platelet aggregation. CD39-L4 protein has 30% and 80% homology to human and murine CD39-L4 is used to treat or prevent thrombosis, myocardial infarction, cerebral ischaemia and angina. It is also used in vitro, to maintain vascular grafts or during extracorporeal circulation, to hydrolyse NDP, as molecular weight markers and as nutritional supplements. It is used to adentify therapeutic agents that bind and modulate CD39-L4. It is coupled to toxins for targeting drugs to tumours or other cells that express CD39
 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419
 AVDIDMIDYEKGGILKVEDFERKAREVCDNLENFISGSPFLCMDLSYITALLKDGFGFAD 395
 nucleic acid encoding human CD39-like protein, useful for treating preventing thrombotic disease.
 40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ
 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD
 LQASPEGYLTALRMFNRTYKLYSYSYLGLGLMSARLA1LGGVEGQPAKDGKELVSPCLSP
 LEQTPRGYLTSFEMFNSTYKLYTHSYLGFGLKAARLATLGALETE-GTDGHTFRSACLPR
 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL
 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
 FLVPKGSVSIMDGSDEGILAWVIVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT
 Gaps
 . 9
 Length 428;
 Indels
 199. .206
/note= "Conserved motif in ATPDases"
 42.3%; Score 999; DB 3; L
52.4%; Pred. No. 8.6e-86;
ive 56; Mismatches 123;
/label= Apyrase_Conserved_Region
 Claim 15; Fig 2; 125pp; English
 98US-00118205.
98US-00122449.
99US-00244444.
99US-00273447.
 99WO-US016180
 N-PSDB; AAZ50356, AAZ50359.
 Best Local Similarity 52.49
Matches 204; Conservative
 2000-182397/16
 INC.
 Mulero J;
 nucleic acid
 AA;
 WO200004041-A2
 (HYSE-) HYSEQ
 Sequence 428
 16-JUL-1998;
24-JUL-1998;
04-FEB-1999;
 16-JUL-1999;
 09-JUL-1999;
 19-MAR-1999
 27-JAN-2000
 157
 217
 121
 301
 276
 361
 62
 241
 Query Match
 181
 Ford J,
 Region
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4,

180 156 240 216

96

300

275

360

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Gaps

9

Length 428 Indels

; Score 999; DB 4; L; Pred. No. 8.6e-86; 56; Mismatches 123;

42.3%; 52.4%;

Query Match 42.3\* Best Local Similarity 52.4\* Matches 204; Conservative

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120

PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 

121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 97 PKQGAETVQGLLEVAKDSIPRSHWKKTPVVLKATAGLRLLPEHKAKALLFEVKEIFRKSP FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT

96

180 156 300

241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 276 WLEAEWIFGGVKYQYGGNQEGEVGFEPCYAEVLRVVRGKLHQPEEVQRGSFYAFSYYYDR 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR

181

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336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSFFLCMDLSYITALLKDGFGFAD 395

448

396 STVLQLTKKVNNIETGWALGATFHLLOSL SKVLKLTRKIDNVETSWALGAIFHYIDSL

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AAB72243 standard; protein; 428

RESULT 15

AAB72243

(first entry)

14-MAY-2001

AAB72243;

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This invention relates to polynuclectides encoding human CD39-like

CD polypeptides with apyrase and/or NDPase activity. The polypeptides having
ATPDAse, including NDPase, activity are useful for inhibiting platelet

C function and can therefore be used in the prophylaxis or treatment of

pathological conditions caused by or involving thrombosis or excessive

CC dagulation or excessive platelet aggregation, such as myocardial

infarction, cerebral ischeamia, angina, arterial thrombosis, cerebral

c infarction, cerebral ischeamia, angina, arterial thrombosis, cerebral

artery thrombosis or intracardiac thrombosis, and conditions associated

with venous thrombosis. CD39-L4 and CD39-L2 polypeptides are useful in

c modulating disease states (including platelet aggregation, inflammation

and apoptosis) associated with ADP or other purinergic signalling by

creducing the levels of NDPs. The polypeptides are also useful for

prophylaxis or treatment of inflammation related disorders, such as

creducing the levels of NDPs. The polypeptides are also useful for

prophylaxis or treatment of inflammation related disorders, such as

cytokine overstimulation); autoimmune adisorders as thrombosis,

cytokine overstimulation); autoimmune adisorders such as thrombosis,

cytokine overstimulation); autoimmune adisorders such as thrombosis,

cytokine overstimulation); autoimmune adisorders such as thromposis,

cytokine overstimulation); autoimmune adisorders such as thrombosis,

cytokine overstimulation; autoimmune adisorders, architis;

corrhosis, reperfusion injury, asthma, multiple sclerosis, arthritis;

corrhosis, and amyotrophic lateral sclerosis, and cancer. The present

cytokine oversion, Albabeimer's disease, parkinson's disease, Huntington's

correspondence represents human CD39 like protein CD39-L4
 WO200110205-A1.
 09-AUG-2000;
 11-JAN-2000;
25-APR-2000;
 09-AUG-1999;
 Homo sapiens
 14-MAY-2001
 15-FEB-2001
 AAB72238
 Ford J,
AAB7223
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```
Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDPase activity, which are useful in the treatment of pathological conditions caused by thrombosis (e.g. myocardial infarction) and
 Human CD39-like protein, apyrase, NDPase, platelet function inhibitor, myocardial infarction; cerebral ischaemia, angina, arterial thrombosis, cerebral artery thrombosis, platelet aggregation; inflammation, apoptosis, autoimmune disorder; neurological disorder, Alzheimer's disease, Parkinson's disease, cancer; CD39-L4.
 Human CD39 like protein CD39-L4 amino acid sequence.
 396 STVLQLTKKVNNIETGWALGATFHLLOSL 424
420 SKVLKLTRKIDNVETSWALGAIFHYIDSL
 Claim 15; Fig 2; 203pp; English.
 AAB72238 standard; protein; 428
 Ö
 2000US-00481238.
2000US-00557800.
 2000WO-US021790
 99US-00370265
 26-MAY-2000; 2000US-00583231.
 Yeung
 (first entry)
 Mulero JJ,
 WPI; 2001-147489/15.
 (HYSE-) HYSEQ INC
 N-PSDB; AAF63383
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Polynucleotides encoding human CD39-like polypeptides, with apyrase and/or NDPase activity, which are useful in the treatment of pathological
 myocardial infarction, cerebral ischaemia, angina, arterial thrombosis; cerebral artery thrombosis, platelet aggregation; inflammation; apoptosis, autoimmune disorder; neurological disorder; Alzheimer's disease; Parkinson's disease; cancer; CD39-L4.
 Human CD39-like protein; apyrase; NDPase; platelet function inhibitor;
 Human CD39 like protein CD39-L4 amino acid sequence.
 11-JAN-2000; 2000US-00481238.
25-APR-2000; 2000US-00557800.
26-MAY-2000; 2000US-00583231.
30-UUN-2000; 2000US-0068283.
 ö
 09-AUG-2000; 2000WO-US021790
 99US-00370265
 Yeung
 Ford J, Mulero JJ,
 2001-147489/15.
 (HYSE-) HYSEQ INC
 N-PSDB; AAF63402
 WO200110205-A1.
 09-AUG-1999;
 Homo sapiens
 15-FEB-2001
HAX BEX LIX BY SERVE ```

Sequence 428 AA;

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conditions caused by thrombosis (e.g. myocardial infarction) and
                                              inflammatory disorders.
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9; Page 142-144; 203pp; English.

This invention relates to polymucleotides encoding human CD39-like

polypeptides with apyrase and/or NDPase activity. The polypeptides having

the APPDase, including NDPase, activity are useful for inhibiting platelet

tunction and can therefore be used in the prophylaxis or treatment of

tunction and can therefore be used in the prophylaxis or treatment of

capulation or excessive platelet aggregation, such as myocardial

infarction, cerebral ischaemia, angina, arterial thrombosis or excessive

coagulation or excessive platelet aggregation, such as myocardial

artery thrombosis or intracardia chrombosis, and conditions associated

with venous thrombosis. CD39-14 and CD39-L2 polypeptides are useful in

modulating disease states (including platelet aggregation, inflammation

complyations or treatment of inflammation related disorders, such as

correction to recentively in the polypeptides are also useful for

correction the levels of NDPs. The polypeptides are also useful for

correction associated conditions such as fever, tachycardia, tachypnea,

correction overstimulation); autoimmune disorders such as thrombosis,

correction overstimulation); autoimmune disorders such as thrombosis,

correctionsis, reperfusion injury, asthma, multiple sclerosis, arthritis;

contrological disorders including neurodegenerative diseases, epilepsy,

disease, and amyotrophic lateral sclerosis, and cancer. The present

corrections and amyotrophic lateral sclerosis, and cancer. The present

Sequence 428 AA;

156 62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGIRLLPGEKAQKILQKVKEVFKASP 180 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT 240 241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419 336 AVDTDMIDYEKGGILKVEDFERRAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395 40 PINVSA---STLYGIMFDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ 96 6; Gaps Length 428; Query Match 42.3%; Score 999; DB 4; Length 42 Best Local Similarity 52.4%; Pred. No. 8.6e-86; Matches 204; Conservative 56; Mismatches 123; Indels SKVLKLTRKIDNVETSWALGAIFHYIDSL 448 181 157 420 dd g δ g à g ð a à 원 ð ö

Search completed: November 16, 2004, 16:56:11 Job time : 160 secs

STVLQLTKKVNNIETGWALGATFHLLOSL 424

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(without alignments)
1136.208 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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length: 2000000000
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SUMMARIES		ID	US-10-092-063-27	US-10-286-926-27	US-10-231-913-123	US-10-231-913-36	US-10-231-913-124	US-10-231-913-38	US-10-231-913-125	US-10-231-913-271	US-10-231-913-126	US-10-091-085-3	US-10-091-085-5	US-10-092-063-3	US-10-092-063-5
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14 US-10-286-926-3	14 US-10-286-926-5	15 US-10-231-913-127	13 US-10-091-085-7		14 US-10-286-926-7	16 US-10-408-765A-2296	13 US-10-092-063-25		13 US-10-092-063-39	9 US-09-925-299-876	10 US-09-925-299-876	4	9 US-09-129-112-19	15 US-10-425-114-36762	14 US-10-369-493-2169	9 US-09-129-112-2	LS US-10-425-114-45875	US-09-129-112-9	17 US-10-425-115-334052	.5 US-10-424-599-230158	14 US-10-369-493-1713		.5 US-10-425-114-49933	.7 US-10-425-115-185050	.5 US-10-425-114-51762	.5 US-10-424-599-145076	.5 US-10-231-913-272	.7 US-10-739-930-10227	US-09-129-112-15	-425-11	-115-21311
428	428	428	428 1	428	428 1	428 1	405 1	405 1	465 1	330 5	330 1	•		433 1	556 1	462 9	467 1	459 9	562 1	467 1	518 1	534 1	443 1	464 1	457 1	459 1	410 1	469 1	462 9	516 1	463 1
42.3	42.3	42.3	42.1	42.1	42.1	42.0	38.5	38.5	38.5	34.8	34.8	25.0	22.2	21.5	21.5	21.4	21.3	21.2	21.2	21.2	21.1	20.8	20.7	20.7	20.4	20.4	20.5	19.8	19.6	19.1	18.9
666	666	666	966	966	966	992	606	606	606	823	823	590.5	525.5	508.5	508	206	504	501	500.5	200	498	491	490.5	489	483	483	478.5	467	463	452.5	447
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ALIGNMENTS

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Sequence 27, Application US/10092063
Sequence 27, Application US/10092063
Fublication No. US20020173005A1
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Ford, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REPRENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/10/092,063
FURRENT FILING DATE: 2002-03-05
FRIOR APPLICATION NUMBER: 09/370,265
FRIOR APPLICATION NUMBER: 09/370,265
FRIOR APPLICATION NUMBER: 09/370,463
FRIOR FILING DATE: 1999-07-16
FRIOR FILING DATE: 1999-02-04
FRIOR FILING DATE: 1999-02-04
FRIOR FILING DATE: 1999-02-04
FRIOR FILING DATE: 1999-02-04
FRIOR PRIOR FILING DATE: 1999-02-04
FRIOR FILING DATE: 1999-07-16
FRIOR APPLICATION NUMBER: 09/118,205
FRIOR FILING DATE: 1999-07-16
FRIOR APPLICATION NUMBER: 09/118,205
FRIOR FILING DATE: 1999-07-16
FRIOR APPLICATION NUMBER: 09/118,205
FRIOR FILING DATE: 1999-07-16
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Query Match

Best Local Similarity 100.0%; Pred. No. 8.7e-218;

Matches 456; Conservative 0; Mismatches 0; Indels 0;
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US-10-092-063-27
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us-09-905-589a-2.rapb

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Best_Local Similarity
Matches 456; Conserv
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                                           29 MRXISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REPRENDATE: 2010/3645/CO/
CURRENT APPLICATION NUMBER: US/10/286,926
CURRENT PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/481,285
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
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SEQ ID NO 27
LENGTH: 484
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                                                                                                                                                                                                                                                                                                                                                                                        FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
                                                                                                                                       29 MRKISNHGSLRVAKVAXPLGLCVGVFIXVAXIKWHRATATQAFFSITRAAFGARWGQQAH
                                                                                                                                                                                            61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD
                                                                                               1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH
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tch 100.0%; Score 2364; DB 14; Length 484; al Similarity 100.0%; Pred. No. 8.7e-218; 456; Conservative 0; Mismatches 0; Indels 0;
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APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456
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UNERROW PEPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR PLING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 123, Application US/10231913; Publication No. US20040005576A1; GENERAL INFORMATION:
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Shimkets, Richard A.
Casman, Stacle J.
Malyankar, Uriel M.
Tohernev, Velizar T.
Vernet, Corine A.
Spytek, Kimberly A.
Shenoy, Sureah G.
Alsobrook II, John P.
Belinger, Schlomit
Peyman, John A.
Stone, David J.
Ellerman, Karen
Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
Eisen, Andrew J.
Liu, Xiaohong
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APPLICANT: STUER, LOYAL O. APPLICANT: STUERMAN, KAREN APPLICANT: Boldon, Ference L. APPLICANT: Boldon, Ference D. APPLICANT: Boldon, Kachong APPLICANT: Liu, Kachong APPLICANT: Spaderra, Steven K. APPLICANT: Spaderra, Steven K. APPLICANT: Spaderra, Steven K. APPLICANT: Spaderra, Steven C. TILE REFERENCE: 21402-216

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-216

CURRENT FILING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: 60/25,029

PRIOR PELING DATE: 2001-01-24

PRIOR PELING DATE: 2001-01-25

PRIOR PELING DATE: 2001-01-25

PRIOR PELING DATE: 2001-01-24

PRIOR PELING DATE: 2001-01-25

PRIOR PELING DATE: 2001-01-25

PRIOR PELING DATE: 2001-01-25

PRIOR PELING DATE: 2001-01-25

PRIOR PELING DATE: 2001-03-26

PRIOR PELING DATE: 2001-03-26

PRIOR PELING DATE: 2001-03-27

PRIOR PELING DATE: 2001-03-27

PRIOR PELING DATE: 2001-03-27

PRIOR PELING DATE: 2001-03-21

SOSTWARER PERENCE PALENTIN VET: 2.1
                                                Peyman, John A.
Stone, David J.
Bllerman, Karen
Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
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Best Local Similarity 99.8%;
Matches 455; Conservative
                             Edinger, Schlomit
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US-10-231-913-36
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PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/266,942
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-24
PRIOR PLING DATE: 2001-04-24
PRIOR PLING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2001-09-12
SEQ ID NO 5: 292
SOFTWARE: PARCHILIN VEY: 2.1
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Sequence 36, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Gi, Li,
APPLICANT: Bit, Li,
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0°
Best Local Similarity 100.0°
Matches 456; Conservative
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; ORGANISM: Homo sapiens
US-10-231-913-123
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61 SPLGTAADGHEVFYGIMFDAGSTGTRVHVFQFTRPPRETPTLTHETFKAVKPGLSAYADD 120 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180 240 300 361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRILETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420 371 431 1 MRKISNHGSLRVAKVAYPLGLCVGVFIYVAYIKWHRATATQAFFSITRAAPGARWGQQAH 241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 301 SFKGEWEHAEVTYRVSGOKAAASLHELCAARVSEVLONRVHRTEEVKHVDFYAFSYYYDL 372 AAGVGLIDAEKGGSLUVGDFELAAKYVCRTLETQPQSSSPFSCMDLTYVSLLLQEFGFPRS FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 312 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL .. Length 467; Indels Score 2361; DB 15; Pred. No. 1.6e-217; 1; Mismatches 0; 421 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 456 420

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268 300

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269 IQASPPGYLTALRMFNRTYKLYSYSYLGLGTMSARLAILGGVEGQPAKDGKELVSPCLSP 328
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                                                                                                                                                                                                                                                                                                                                                                                                 389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 448
241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP
                                                                                                                                                                                                                                                                                                                                                                   361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
                                                                         181 FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT
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APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
ATITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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FILE REPERENCE: 21402-216

CURRENT APPLICATION NUMBER: US/10/21,913

CURRENT FILING DATE: 2002-08-30

PRIOR PEDICATION NUMBER: 60/25,029

PRIOR PELING DATE: 2000-12-06

PRIOR PELING DATE: 2000-12-12

PRIOR PELING DATE: 2000-12-12

PRIOR PELING DATE: 2001-10-08

PRIOR FILING DATE: 2001-01-08

PRIOR PELING DATE: 2001-02-20

PRIOR PELING DATE: 2001-02-20

PRIOR PELING DATE: 2001-02-20

PRIOR PELING DATE: 2001-02-20

PRIOR PELING DATE: 2001-04-24

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PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
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Eisen, Andrew J.
Liu, Xiaohong
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Gangolli, Esha A.
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CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR PELING DATE: 2000-12-06
PRIOR PELING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/250,326
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR PILING DATE: 2001-01-06
PRIOR PILING DATE: 2001-01-06
PRIOR PILING DATE: 2001-01-07
PRIOR PELING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR PELING DATE: 2001-09-12
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               432 KVLKLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 467
                                                                                                                                                                 Sequence 124, Application US/10231913 publication No. US20040005576A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Vernet, Corine A.
Spytek, Kimberly A.
Shenoy, Suresh G.
Alsobrook II, John P.
Bedinger, Schlomit
Peyman, John A.
Stone, David J.
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Padigaru, Muralidhara
Spaderna, Steven K.
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Shimkets, Richard A
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Tchernev, Velizar T
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Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
Eisen, Andrew J.
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SEQ ID NO 124
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ORGANISM: Homo sapiens
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301 SFKGEWEHAEVTYRVSGQKAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.3%; Score 2063.5; DB 15
86.6%; Pred. No. 5.7e-189;
ative 27; Mismatches 33;
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                       CURRENT APPLICATION NUMBER: US/10/231,9
CURRENT FILING DATE: 2002-08-30
PRIOR PILING DATE: 2000-18-30
PRIOR PELLING DATE: 2000-18-30
PRIOR PELLING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/25,029
PRIOR PILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR PILING DATE: 2001-01-24
PRIOR PELLING DATE: 2001-01-24
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR PILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/319,627
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
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APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 394; Conservative
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Best Local Similarity
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                                                                                                                               Length 446;
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                Indels
                                                                                                                          89.5%; Score 2116; DB 15;
ilarity 91.0%; Pred. No. 5.1e-194;
Conservative 1; Mismatches 2;
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                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                              29 MRKISNHGSLRVAV------
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Publication No. US20040005576Al
GENERAL INFORMATION:
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Spaderna, Steven K.
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; SOFTWARE: Patentin Ver. 2; SEQ ID NO 38; LENGTH: 446; TYPE: PRT; ORGANISM: Homo sapiens US-10-231-913-38
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Best Local Similarity
Matches 415; Conserv
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85 TRVHVEQFT-RPPRETPTLTHETFKAVKPGLSAYADDVEKSAQGIRELLDVAKQDIPFDF 143
301 KGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRSKVLKLTRKID 360
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CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-08
PRIOR FILING DATE: 2001-0-08
PRIOR FILING DATE: 2001-0-08
PRIOR FILING DATE: 2001-0-08
PRIOR FILING DATE: 2001-0-1-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR APPLICATION NUMBER: 60/269,183
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR PRILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR APPLICATION NUMBER: 60/318,712
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Sequence 126, Application US/10231913
Publication No. US20040005576A1
GRNERAL INFORMATION:
                                                  431 NVETSWALGAIFHYIDSLN 449
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Tchernev, Velizar T.
Vernet, Corine A.
Spytek, Kimberly A.
Shenoy, Suresh G.
Alsobrook II, John P.
Edinger, Schlomit
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Stone, David J.
Ellerman, Karen
Gangolli, Esha A.
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APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
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Colman, Steven D.
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SEQ ID NO 126
LENGTH: 427
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APPLICANT:
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Pred. No. 1.4e-178;
1; Mismatches 0; Indels 0
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APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
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PRIOR APPLICATION NUMBER: 60/251,660
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR PILING DATE: 2000-12-06
PRIOR PILING DATE: 2000-12-02
PRIOR PAPLICATION NUMBER: 60/263,029
PRIOR PILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-01-24
PRIOR PILING DATE: 2001-03-26
PRIOR PILING DATE: 2001-03-24
PRIOR PILING DATE: 2001-04-24
PRIOR PILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
NUMBER OF SEQ ID NOS: 292
                                                                            Vernet, Corine A.
Spytek, Kimberly A.
Shenoy, Suresh G.
Alsobrook II, John P.
Edinger, Schlomit
Peyman, John A.
Stone, David J.
Ellerman, Karen
Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
Eisen, Andrew J.
Liu, Xiaohong
Padigaru, Muralidhara
                                      Malyankar, Uriel M.
Tchernev, Velizar T.
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Best Local Similarity 99.7
Matches 378; Conservative
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ORGANISM: Homo sapiens
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301 SFKGEWEHAEVTYRVSGOKAAASLHELCAARVSEVLONRVHRTEEVKHVDFYAFSYYYDL 360
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APPLICANT: Ford, John
APPLICANT: Ford, John
TILE OF INVENTION: MALEAC, JULIO
TILE OF INVENTION: MATCHOOS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TILLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/35761
CURRENT APPLICATION NUMBER: 09/350,836
FRIOR FILING DATE: 1999-07-09
FRIOR FILING DATE: 1999-07-06
FRIOR FILING DATE: 1999-02-04
                                                                                                                                             157 FLVPKGSVSIMDGSDEGILAWTVNFLTGQLHGHRQETVGTLDLGGASTQITFLPQFEKT
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                                                                                                                                                                                                                                                                                                             SKVLKLTRKIDNVETSWALGAIFHYIDSL 448
                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10091085
Publication No. US20020146772A1
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Best Local Similarity 52.4%;
Matches 204; Conservative 56
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Best Local Similarity
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TRIHVYTFVQKTAGQLPFLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSH 118
                                                                                                                                                                                      179 VNFLTGQLHGRGQETVGTLDLGGASTQITFLPQFEKTLEQTPRGYLTSFEMFNSTFKLYT 238
                                                                                                                                                                                                                                            264 YSYLGLGLMSARLALLGGVEGQPAKDGKELVSPCLSPSFKGEWEHAEVTYRVSGQKAAAS 323
                                                                                                                                                                                                                                                                                                                                           324 LHELCAARVSEVLONRVHRTEEVKHVDFYAFSYYYDLAAGVGLIDAEKGGSLVVGDFEIA 383
                                                                                                                                                                                                                                                                                                                                                                          121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
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APPLICANT: Ford, John
APPLICANT: Malero, Julio
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
TITLE OF INVENTION: MCD072
FILE REFERENCE: 28110/35761
CURRENT PEPLICATION NUMBER: US/10/091,085
FILE REFERENCE: 28110/35761
CURRENT FILING DATE: 1002-03-05
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR PELING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-24
PRIOR FILING DATE: 1999-07-24
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-02-04
SPRIOR FILING DATE: 1999-02-04
SPRIOR FILING DATE: 1999-02-04
SPRIOR FILING DATE: 1999-02-04
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                                                                                                                                             204 INFLIGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGTLQASPPGYLTALRMFNRTYKLYS
                                                                                                                                                                                                                                                                           AKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPRSKVLKLTRKIDNVETSWALGAIF
                                                WKATPLVLKATAGLRLLPGEXAQKLLQKVKEVFKASPFLVGDDCVSIMNGTDEGVSAWIT
                                                                          FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGGSTQIAFLPRVEGT
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Publication No. US20020146772A1
GENERAL INFORMATION:
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Sequence 5, Application US/10092063

Sublication No. US2020173005A1

GENERAL INFORMATION:

APPLICANT: FOR JULIO

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

FILE REFERENCE: 2011-035908

CURRENT FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US/10/092,063

CURRENT FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: DE7/US99/16180

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-04

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-07-16

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO S
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; Pred. No. 8.8e-87;
56; Mismatches 123; Indels
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Sequence 3, Application US/10286926

Publication No. US20030175752A1

GENERAL INFORMATION:

APPLICANT: Ford, John

MAPPLICANT: Mulero, Julio
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Best Local Similarity 52.49
Matches 204; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
CURRENT STILE OF TWENTIONS METHADS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REFERENCE: 2810/35908
CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT APPLICATION NUMBER: 09/370,265
PRIOR PLILNG DATE: 1099-07-13
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-07-04
PRIOR PAPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-07-24
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336 AVDTDMIDYEKGGILKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFAD 395
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                                                       420 SKVLKLTRKIDNVETSWALGAIFHYIDSL
                                                                                                                                                                                                                               Sequence 3, Application US/10092063; Publication No. US20020173005A1; GENERAL INFORMATION:
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INVENTION: Methods and Materials Relating to CD39-Like
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APPLICANT: Yeung, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 42.3%; Score 999; DB 14; Length 428; al Similarity 52.4%; Pred. No. 8.8e-87; 204; Conservative 56; Mismatches 123; Indels
                                        TITLE OF INVENTION: INCLINIOL AND ADDRESS 
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; ORGANISM: Homo sapiens
US-10-286-926-3
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LENGTH: 428
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Sequence 5, Application US/10286926 Publication No. US20030175752A1 GENERAL INFORMATION: APPLICANT: Ford, John APPLICANT: Mulero, Julio APPLICANT: Yeung, George

US-10-286-926-5

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241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
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52.4%; Pred. No. 8.8e-87;
tive 56; Mismatches 123;
TITLE OF INVENTION: Methods and Materials Relatine OF INVENTION: Polypeptides
FILE REPERENCE: 28110/36457CON
CURRENT APPLICATION NUMBER: US/10/286,926
CURRENT FILING DATE: 2002.11-01
PRIOR APPLICATION NUMBER: 09/55,800
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-07-09
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Job time : 144 secs
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Matches 204; Conservative
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US-10-286-926-5
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ORGANISM: Homo sapiens
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US-09-240-639-9

US-09-350-888-5

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                                        GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240, 639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 2.0
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Sequence 2, Application US/09240639 Patent No. 6350447
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/10/107,660
CURRENT PILIG DATE: 2002-03-27
PRIOR PILIGATION NUMBER: US/09/240,639
PRIOR FILING DATE: 1998-01-29
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE IIILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/905,744
CURRENT APPLICATION NUMBER: US/09/905,744
FILING DATE: 2001-07-13
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 456
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US-10-107-660-2
Sequence 2, Application US/10107660
Patent No. 6780977
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 456; Conservative
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CRGANISM: Homo sapiens
US-09-905-744-2
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Sequence 2, Application US/09908510A

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Sequence 2, Application US/09908510A

GREEAL INFORMATION:

APPLICANT: Chadwick, Brian Paul

APPLICANT: Chadwick, Brian Paul

APPLICANT: Frischauf, Anna Maria

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND

TITLE OF INVENTION: AGIDS

FILE REPERENCE: 28110/36120B

CURRENT APPLICATION NUMBER: US/09/908,510A

CURRENT APPLICATION NUMBER: 09/240,639

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1

SEQ ID NO 2.
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Frischauf, Anna-Maria
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ORGANISM: Homo Sapiens
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, APPLICANT: Chadwick,
, APPLICANT: Frischauf
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US-09-905-744-2
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SOFTWARE: Patentin Ver. 2.0
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100.0%; Score 2364; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.1e-230;
Matches 456; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Frischauf Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING T
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/10/107,576
CURRENT PILING DATE: 2002-03-27
PRIOR PILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 2
         100.0%; Score 2364; DB 4;
100.0%; Pred. No. 1.1e-230;
iive 0; Mismatches 0;
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US-10-107-576-2
Sequence 2, Application US/10107576
; Patent No. 6783959
         Query Match
Best Local Similarity 100.
Matches 456; Conservative
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ORGANISM: Homo sapiens
US-10-107-576-2
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269 IQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 328
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Sequence 27. Application US/09370265
Patent No. 6447771
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: MITCHO, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
FILE OF INVENTION: POLYPEPTIDES
FILE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 2811/155908
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT APPLICATION NUMBER: US/09/370,265
CURRENT PILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 09/236,836
EARLIER APPLICATION NUMBER: 09/234,444
EARLIER PELING DATE: 1999-07-09
EARLIER PELING DATE: 1999-07-09
EARLIER PELING DATE: 1999-07-09
EARLIER PELING DATE: 1999-07-04
EARLIER PELING DATE: 1999-07-16
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Best Local Similarity 100.
Matches 456; Conservative
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US-09-370-265-27
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                                                                              361 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS 420
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## PERENTER NO. 9539013
## APPLICANT: POTCH, John
## APPLICANT: POTCH, JUNIO
## APPLICANT: POTCH, JUNIO
## APPLICANT: POTCH, JUNIO
## APPLICANT: POTCH, JUNIO
## APPLICANT: POTCH ## APPLICANTON: POLYPEPTIDES
## TITLE OF INVENTION: POLYPEPTIDES
## TITLE OF INVENTION: POLYPEPTIDES
## FILE REPRENCE: 28110/36570
CURRENT APPLICATION NUMBER: U$/09/608,285A
## PRIOR APPLICATION NUMBER: 09/537,800
## PRIOR FILING DATE: 2000-06-26
## PRIOR FILING DATE: 2000-04-25
## PRIOR PELING DATE: 1099-004-25
## PRIOR PELING DATE: 1999-08-09
## PRIOR PELING DATE: 1999-07-16
## PRIOR PELING DATE: 1999-02-04
## PRIOR PELING DATE: 1999-07-16
## PRIOR PEL
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100.0%; Pred. No. 1.2e-230;
tive 0; Mismatches 0;
                                                                                                                                                                                                       KVLKLTRKI DNVETSWALGAI FHY I DSLNRQKSPAS
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/09608285A
Patent No. 6335013
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US-09-608-285A-27
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PACENTAL INCORMATION:
APPLICANT: Ford, John
APPLICANT: Ford, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REPERENCE: 28110/35908
CURRENT APPLICATION NUMBER: U5/09/370,625A
CURRENT PILING DATE: 1999-08-09
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1999-07-16
PRIOR PELING DATE: 1999-07-09
      389 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLILLQEFGFPRS 448
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                                                                                                                                                                                                                                    Sequence 27, Application US/09370625A
Patent No. 6600032
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Matches 456; Conservative
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                                                    AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQEFGFPRS
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                                                                                                 KVLKLTRKIDNVETSWALGAIFHYIDSLNROKSPAS 456
                                                                                                                  449 KVLXLTRKIDNVETSWALGAIFHYIDSLNRQKSPAS 484
                                                                                                                                                                                                        Sequence 27, Application US/09557800C Patent No. 6476211
GENERAL INFORMATION:
APPLICANT: FORd, John APPLICANT: Muleco, Julio APPLICANT: Yeung, George
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Matches 456; Conservative 0
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; ORGANISM: Homo sapiens
US-09-557-800C-27
                                  361
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APPLICANT: FORG, JOHN
APPLICANT: FORG, JOHN
APPLICANT: Wile CAST
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/587,800
PRIOR APPLICATION NUMBER: 09/587,800
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/587,800
PRIOR PILING DATE: 2000-04-25
PRIOR PELING DATE: 1099-08-09
PRIOR PILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/344,444
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR APPLICATION NUMBER: 09/244,444
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR APPLICATION NUMBER: 09/122,449
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1998-07-16
PRIOR FILING DATE: 1998-07-16
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| ||:||:||:|| ||||| || : ||
                                             Sequence 3, Application US/09608285A
Patent No. 6335013
GENERAL INFORMATION:
APPLICANT: Ford, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 42.3%; sal Similarity 52.4%; 204; Conservative 56
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US-09-608-285A-3
                  JS-09-608-285A-3
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SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP
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                                                               FRIEND NO. 6335013

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Milero, Julio

TITLE OF INVENTION: MCPEPTIDES

TITLE OF INVENTION: POLYEBTIDES

TITLE OF INVENTION: POLYEBTIDES

CURRENT APPLICATION NUMBER: US/09/608,285A

CURRENT APPLICATION NUMBER: 09/557,800

FRIOR FILING DATE: 2000-06-26

FRIOR APPLICATION NUMBER: 09/481,238

FRIOR APPLICATION NUMBER: 09/481,238

FRIOR FILING DATE: 1999-00-09

FRIOR FILING DATE: 1999-00-09

FRIOR FILING DATE: 1999-07-06

FRIOR FILING DATE: 1999-07-09

FRIOR FILING DATE: 1999-07-09

FRIOR FILING DATE: 1999-07-09

FRIOR FILING DATE: 1999-07-09

FRIOR FILING DATE: 1999-07-04

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                        Sequence 60, Application US/09608285A Patent No. 6335013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.5
Matches 388; Conservative
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JS-09-608-285A-60
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62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120 240 LOASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300 301 SFKGEWEHAEVTYRVSGQXAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360 AAGVGLIDAEKGGSLVVGDFEIAAKYVCRTLETQPQSSPFSCMDLTYVSLLLQE-FGFPR 419 121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP FLVGDDCVSIMNGTDEGVSAWITINFLTGSLKTPGGSSVGMLDLGGGSTQIAFLPRVEGT 40 PINVSA---STLYGIMPDAGSTGTRIHVYTFVQKMPGQLPILEGEVFDSVKPGLSAFVDQ Gaps 9 ; Score 999; DB 3; Length 42; Pred. No. 2.2e-92; 56; Mismatches 123; Indels

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62 PLGTAADGHEVFYGIMFDAGSIGIRVHVFQFT-RPPREIPTLIHETFKAVKPGLSAYADD 120
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                                                                                                                                                                                                                       APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: MTHODS AND COMPOSITIONS RELATING TO CD39-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REPERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 428
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Patent No. 6350447
GENERAL INFORMATION
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
FILE REPERBNCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT APPLICATION NUMBER: US/09/240,639
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.3%; Score 999; DB 3; E 52.4%; Pred. No. 2.2e-92; tive 56; Mismatches 123;
              396 STVLQLTKKVNNIETGWALGAFFHLLQSL 424
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                                                                                                                                                                         ; Sequence 6, Application US/09240639; Patent No. 6350447
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Best Local Similarity 52.4%
Matches 204; Conservative
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US-09-240-639-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 SFKGEWEHAEVTYRVSGOKAAASLHELCAARVSEVLONRVHRTEEVKHVDFYAFSYYYDL 360
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APPLICANT: Ford, John
APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Wulero, Julio
TITLE OF INVENTION: POLYPEPTIDES
FILE REPRENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-36
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR PILING DATE: 1999-07-16
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42.3%; Score 999; DB 3; Length 428;
Best Local Similarity 52.4%; Pred. No. 2.2e-92;
Matches 204; Conservative 56; Mismatches 123; Indels
396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
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                                                                                                                                    Sequence 5, Application US/09608285A
Patent No. 6335013
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ORGANISM: Homo sapiens
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SEQ ID NO 5
LENGTH: 428
                                                                                                          US-09-608-285A-5
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121 VEKSAQGIRELLDVAKQDIPFDFWKATPLVLKATAGLRLLPGEKAQKLLQKVKEVFKASP 180
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                                                                                                                                                                                                                241 LQASPPGYLTALRMFNRTYKLYSYSYLGLGLMSARLAILGGVEGQPAKDGKELVSPCLSP 300
                                                                                                                                                                                                                                                                   336 AVDIDMIDYEKGGILKVEDFERKAREVCDNLENFISGSPFLCMDLSYITALLKDGFGFAD 395
                                                                                                  62 PLGTAADGHEVFYGIMFDAGSTGTRVHVFQFT-RPPRETPTLTHETFKAVKPGLSAYADD 120
                                                                                                                                                                 301 SFKGEWEHAEVTYRVSGQXAAASLHELCAARVSEVLQNRVHRTEEVKHVDFYAFSYYYDL 360
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                Query Match 42.3%; Score 999; DB 3; Length 428; Best Local Similarity 52.4%; Pred. No. 2.2e-92; Matches 204; Conservative 56; Mismatches 123; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    396 STVLQLTKKVNNIETGWALGATFHLLQSL 424
; TYPE: PRT
; OKGANISM: Homo sapiens
US-09-240-639-9
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Search completed: November 16, 2004, 17:01:10 Job time : 42 secs